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OM protein - protein search, using sw model

Run on: March 3, 2004, 12:33:10 ; Search time 15.317 Seconds
(without alignments)
734.770 Million cell updates/sec

Title: US-09-825-561A-6
Perfect score: 1195
Sequence: 1 CPDLVCYTDYLTQVICILEM.....SDPVFQTSBELKEGNPH 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1195	100.0	538	3	US-09-040-005-2
2	1195	100.0	538	4	US-09-522-217-115
3	1195	100.0	538	4	US-09-404-641-2
4	1195	100.0	538	4	US-09-923-246-115
5	1195	100.0	538	4	US-10-295-723-115
6	1195	100.0	606	4	US-09-522-217-97
7	1195	100.0	606	4	US-09-404-641-51
8	1195	100.0	606	4	US-09-923-246-97
9	1195	100.0	606	4	US-10-295-723-97
10	844	70.6	529	4	US-09-404-641-85
11	838	70.1	529	4	US-09-732-234-6
12	838	70.1	529	4	US-08-784-859-6
13	400	33.5	397	4	US-09-404-641-81
14	144	12.1	783	4	US-08-780-562-7
15	144	12.1	894	2	US-08-599-455B-2
16	144	12.1	894	3	US-09-069-781B-2
17	144	12.1	894	4	US-08-618-957A-12
18	144	12.1	894	4	US-09-137-132-2
19	144	12.1	894	4	US-08-864-564A-2
20	144	12.1	894	4	US-09-094-410-2
21	144	12.1	894	4	US-08-708-123D-2
22	144	12.1	894	4	US-08-583-153A-2
23	144	12.1	894	4	US-08-570-142D-2
24	144	12.1	894	4	US-08-638-524B-2
25	144	12.1	1162	2	US-08-593-455B-43
26	144	12.1	1162	3	US-09-063-781B-43
27	144	12.1	1162	4	US-09-137-132-43

28	144	12.1	1162	4	US-08-864-564A-43	Sequence 43, Appl
29	144	12.1	1162	4	US-09-094-410-43	Sequence 43, Appl
30	144	12.1	1162	4	US-08-708-123D-43	Sequence 43, Appl
31	144	12.1	1162	4	US-08-638-524B-43	Sequence 12, Appl
32	142.5	11.9	896	2	US-08-640-389A-12	Sequence 12, Appl
33	141.5	11.8	539	6	5198359-4	Patent No. 5198359
34	141.5	11.8	539	6	5449756-4	Patent No. 5449756
35	140.5	11.8	691	4	US-09-313-942-20	Sequence 20, Appl
36	140.5	11.8	694	4	US-09-313-942-22	Sequence 22, Appl
37	140.5	11.8	784	4	US-09-313-942-30	Sequence 30, Appl
38	139	11.6	493	2	US-08-078-311-7	Sequence 7, Appl
39	139	11.6	493	2	US-08-460-402-7	Sequence 7, Appl
40	139	11.6	635	1	US-08-184-327A-4	Sequence 4, Appl
41	139	11.6	635	2	US-08-078-311-1	Sequence 1, Appl
42	139	11.6	635	2	US-08-460-402-1	Sequence 1, Appl
43	139	11.6	635	5	PCT-US95-00670-4	Sequence 4, Appl
44	138	11.5	895	3	US-08-827-962-19	Sequence 19, Appl
45	138	11.5	1162	3	US-08-827-962-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-09-040-005-2
; Sequence 2, Application US/09040005
; Patent No. 6057128
; GENERAL INFORMATION:
; APPLICANT: Donaldson, Debra
; TITLE OF INVENTION: MU-1 RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/040,005
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15320
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-498-8224
; TELEFAX: 617-876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 538 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-040-005-2

Query Match 100.0%; Score 1195; DB 3; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.5e-122; Indels 0; Gaps 0;
Matches 218; Conservative 0; Mismatches 0;
QY 1 CPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDQYELKDEATSCSLHRSAAHATHY 60
DB 20 CPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDQYELKDEATSCSLHRSAAHATHY 79
QY 61 TCHMDVHFMAADDIFSUNITDQSGNYSQCGSFLLAESIKPAPPFNVTFTSGQINISWR 120

Db 80 TCHMDVHFHMADDFSVNITDQSGNYSQCGSFLLAESIKPAPPFNVTTFSGQYNISWR 139
QY 121 SYVEDPAFYMLKGLQYELQYRNRPDPWAVSPRKLISVDSRSVLLPLEFRKDSSEYELQ 180
Db 140 SYVEDPAFYMLKGLQYELQYRNRPDPWAVSPRKLISVDSRSVLLPLEFRKDSSEYELQ 199
QY 181 VRAGPMPGSSYQGTWSEWSDPVIFQTSBELKEGWNPH 218
Db 200 VRAGPMPGSSYQGTWSEWSDPVIFQTSBELKEGWNPH 237

RESULT 2

US-09-522-217-115
; Sequence 115, Application US/09522217
; Patent No. 6307024
; GENERAL INFORMATION:
; APPLICANT: No. 6307024ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: US 60/123,547
; EARLIER FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: US 60/123,904
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: US 60/142,013
; EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-522-217-115

Query Match 100.0%; Score 1195; DB 4; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.5e-122;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDQYEEKDEATCSLHRSAHNATHATY 60
Db 20 CPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDQYEEKDEATCSLHRSAHNATHATY 79
QY 61 TCHMDVHFHMADDFSVNITDQSGNYSQCGSFLLAESIKPAPPFNVTTFSGQYNISWR 120
Db 80 TCHMDVHFHMADDFSVNITDQSGNYSQCGSFLLAESIKPAPPFNVTTFSGQYNISWR 139
QY 121 SYVEDPAFYMLKGLQYELQYRNRPDPWAVSPRKLISVDSRSVLLPLEFRKDSSEYELQ 180
Db 140 SYVEDPAFYMLKGLQYELQYRNRPDPWAVSPRKLISVDSRSVLLPLEFRKDSSEYELQ 199
QY 181 VRAGPMPGSSYQGTWSEWSDPVIFQTSBELKEGWNPH 218
Db 200 VRAGPMPGSSYQGTWSEWSDPVIFQTSBELKEGWNPH 237

RESULT 3

US-09-404-641-2
; Sequence 2, Application US/09404641
; Patent No. 6576744
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.

; APPLICANT: No. 6576744ak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHA11
; FILE REFERENCE: 98-55
; CURRENT APPLICATION NUMBER: US/09/404,641
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-404-641-2

Query Match 100.0%; Score 1195; DB 4; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.5e-122;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 20 CPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDQYEEKDEATCSLHRSAHNATHATY 79
QY 61 TCHMDVHFHMADDFSVNITDQSGNYSQCGSFLLAESIKPAPPFNVTTFSGQYNISWR 120
Db 80 TCHMDVHFHMADDFSVNITDQSGNYSQCGSFLLAESIKPAPPFNVTTFSGQYNISWR 139
QY 121 SYVEDPAFYMLKGLQYELQYRNRPDPWAVSPRKLISVDSRSVLLPLEFRKDSSEYELQ 180
Db 140 SYVEDPAFYMLKGLQYELQYRNRPDPWAVSPRKLISVDSRSVLLPLEFRKDSSEYELQ 199
QY 181 VRAGPMPGSSYQGTWSEWSDPVIFQTSBELKEGWNPH 218
Db 200 VRAGPMPGSSYQGTWSEWSDPVIFQTSBELKEGWNPH 237

RESULT 4

US-09-923-246-115
; Sequence 115, Application US/09923246
; Patent No. 6605272
; GENERAL INFORMATION:
; APPLICANT: No. 6605272ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-15
; CURRENT APPLICATION NUMBER: US/09/923,246
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-246-115

Query Match 100.0%; Score 1195; DB 4; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.5e-122;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCYTDYLTQVICILEMNNLHPSLTTLTWQDYBELKDEATSCSLHSAHNATHATY 60
DB 20 CPDLVCYTDYLTQVICILEMNNLHPSLTTLTWQDYBELKDEATSCSLHSAHNATHATY 79

QY 61 TCHMDVHFHMADDFSVNITDQSGNYSCGSGFLAASIKPAPPFNVTTFSGQYNISWR 120
DB 80 TCHMDVHFHMADDFSVNITDQSGNYSCGSGFLAASIKPAPPFNVTTFSGQYNISWR 139

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QY 181 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
DB 200 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237

RESULT 5
US-10-295-723-115
; Sequence 115, Application US/10295723
; Patent No. 6686178
; GENERAL INFORMATION:
; APPLICANT: No. 6686178ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-723-115

Query Match 100.0%; Score 1195; DB 4; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.5e-122;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCYTDYLTQVICILEMNNLHPSLTTLTWQDYBELKDEATSCSLHSAHNATHATY 60
DB 20 CPDLVCYTDYLTQVICILEMNNLHPSLTTLTWQDYBELKDEATSCSLHSAHNATHATY 79

QY 61 TCHMDVHFHMADDFSVNITDQSGNYSCGSGFLAASIKPAPPFNVTTFSGQYNISWR 120
DB 80 TCHMDVHFHMADDFSVNITDQSGNYSCGSGFLAASIKPAPPFNVTTFSGQYNISWR 139

QY 121 SDYEDPAFYMLKGKLOQYELQYRNRGDPWAVSPRRKLISVDSRSVSLPLFRKDSSEYELQ 180
DB 140 SDYEDPAFYMLKGKLOQYELQYRNRGDPWAVSPRRKLISVDSRSVSLPLFRKDSSEYELQ 199

QY 181 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
DB 200 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237

RESULT 6
US-09-522-217-97
; Sequence 97, Application US/09522217
; Patent No. 6307024
; GENERAL INFORMATION:
; APPLICANT: No. 6307024ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/522,217
; CURRENT FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: US 60/123,547
; EARLIER FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: US 60/123,904
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: US 60/142,013
; EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 97
; LENGTH: 606
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MBP-zalphan1 soluble receptor polypeptide sequence
US-09-522-217-97

Query Match 100.0%; Score 1195; DB 4; Length 606;
Best Local Similarity 100.0%; Pred. No. 1.8e-122;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCYTDYLTQVICILEMNNLHPSLTTLTWQDYBELKDEATSCSLHSAHNATHATY 60
DB 389 CPDLVCYTDYLTQVICILEMNNLHPSLTTLTWQDYBELKDEATSCSLHSAHNATHATY 448

QY 61 TCHMDVHFHMADDFSVNITDQSGNYSCGSGFLAASIKPAPPFNVTTFSGQYNISWR 120
DB 449 TCHMDVHFHMADDFSVNITDQSGNYSCGSGFLAASIKPAPPFNVTTFSGQYNISWR 508

QY 121 SDYEDPAFYMLKGKLOQYELQYRNRGDPWAVSPRRKLISVDSRSVSLPLFRKDSSEYELQ 180
DB 509 SDYEDPAFYMLKGKLOQYELQYRNRGDPWAVSPRRKLISVDSRSVSLPLFRKDSSEYELQ 568

QY 181 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
DB 569 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 606

RESULT 7
US-09-404-641-51
; Sequence 51, Application US/09404641
; Patent No. 6576744
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZALPHA11
; FILE REFERENCE: 98-55
; CURRENT APPLICATION NUMBER: US/09/404,641

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; CURRENT FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 606
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-09-404-641-51

Query Match      100.0%; Score 1195; DB 4; Length 606;
Best Local Similarity 100.0%; Pred. No. 1.8e-122;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCYTDYLTQVICILEMNNLHPSTLTLTWQDQYELKDEATCSLHRSAAHATHATY 60
DB 389 CPDLVCYTDYLTQVICILEMNNLHPSTLTLTWQDQYELKDEATCSLHRSAAHATHATY 448
QY 61 TCHMDVFHFMAADDIFSVNITDQSGNYSQCGSFLAELSIKPAPPNVTVTFSGQYNISWR 120
DB 449 TCHMDVFHFMAADDIFSVNITDQSGNYSQCGSFLAELSIKPAPPNVTVTFSGQYNISWR 508
QY 121 SYEDPAFYMLKGKQYELQYRNRGDPWAVSPRRKLIISVDSRSVSLLEPFKDKSSYELQ 180
DB 509 SYEDPAFYMLKGKQYELQYRNRGDPWAVSPRRKLIISVDSRSVSLLEPFKDKSSYELQ 568
QY 181 VRAGPMGSSYQGTWSESDPVIFQTQSEELKEGWNPH 218
DB 569 VRAGPMGSSYQGTWSESDPVIFQTQSEELKEGWNPH 606

RESULT 8
US-09-923-246-97
; Sequence 97, Application US/09923246
; Patent No. 6605272
; GENERAL INFORMATION:
; APPLICANT: No. 6605272ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Gross, Richard D.
; APPLICANT: Hollis, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHALL LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 97
; LENGTH: 606
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MBP-zalphall soluble receptor polypeptide sequence
US-09-923-246-97

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Query Match      100.0%; Score 1195; DB 4; Length 606;
Best Local Similarity 100.0%; Pred. No. 1.8e-122;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCYTDYLTQVICILEMNNLHPSTLTLTWQDQYELKDEATCSLHRSAAHATHATY 60
DB 389 CPDLVCYTDYLTQVICILEMNNLHPSTLTLTWQDQYELKDEATCSLHRSAAHATHATY 448
QY 61 TCHMDVFHFMAADDIFSVNITDQSGNYSQCGSFLAELSIKPAPPNVTVTFSGQYNISWR 120
DB 449 TCHMDVFHFMAADDIFSVNITDQSGNYSQCGSFLAELSIKPAPPNVTVTFSGQYNISWR 508
QY 121 SYEDPAFYMLKGKQYELQYRNRGDPWAVSPRRKLIISVDSRSVSLLEPFKDKSSYELQ 180
DB 509 SYEDPAFYMLKGKQYELQYRNRGDPWAVSPRRKLIISVDSRSVSLLEPFKDKSSYELQ 568
QY 181 VRAGPMGSSYQGTWSESDPVIFQTQSEELKEGWNPH 218
DB 569 VRAGPMGSSYQGTWSESDPVIFQTQSEELKEGWNPH 606

RESULT 9
US-10-295-723-97
; Sequence 97, Application US/10295723
; Patent No. 6686178
; GENERAL INFORMATION:
; APPLICANT: No. 6686178ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Gross, Richard D.
; APPLICANT: Hollis, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHALL LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 97
; LENGTH: 606
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MBP-zalphall soluble receptor polypeptide sequence
US-10-295-723-97

Query Match      100.0%; Score 1195; DB 4; Length 606;
Best Local Similarity 100.0%; Pred. No. 1.8e-122;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCYTDYLTQVICILEMNNLHPSTLTLTWQDQYELKDEATCSLHRSAAHATHATY 60
DB 389 CPDLVCYTDYLTQVICILEMNNLHPSTLTLTWQDQYELKDEATCSLHRSAAHATHATY 448
QY 61 TCHMDVFHFMAADDIFSVNITDQSGNYSQCGSFLAELSIKPAPPNVTVTFSGQYNISWR 120
DB 449 TCHMDVFHFMAADDIFSVNITDQSGNYSQCGSFLAELSIKPAPPNVTVTFSGQYNISWR 508
QY 121 SYEDPAFYMLKGKQYELQYRNRGDPWAVSPRRKLIISVDSRSVSLLEPFKDKSSYELQ 180
DB 509 SYEDPAFYMLKGKQYELQYRNRGDPWAVSPRRKLIISVDSRSVSLLEPFKDKSSYELQ 568
QY 181 VRAGPMGSSYQGTWSESDPVIFQTQSEELKEGWNPH 218
DB 569 VRAGPMGSSYQGTWSESDPVIFQTQSEELKEGWNPH 606

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FILE REFERENCE: 98-55
CURRENT APPLICATION NUMBER: US/09/404,641
CURRENT FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 60/100,896
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: US 60/123,546
PRIOR FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: US 60/142,574
PRIOR FILING DATE: 1999-07-06
NUMBER OF SEQ ID NOS: 91
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 81
LENGTH: 397
TYPE: PRT
ORGANISM: Mus musculus
US-09-404-641-81

Query Match      33.5%; Score 400; DB 4; Length 397;
Best Local Similarity 68.6%; Pred. No. 1.9e-35;
Matches 72; Conservative 18; Mismatches 15; Indels 0; Gaps 0;

QY 114 QYNISWRSDYEDPAFYMLKGLQYELQYVNRGDPWAVSPRKLISVDSRSVSLPLBFRK 173
DB 1 RYDISWSDAYDEPSNYVLKGLQYELQYVNRGDPWAVSPRKLISVDSRSVSLPLBFRK 60

QY 174 DSSYELQVRAWPGSSYSGTWSWSDPVIPTOTSEELKEGWNPH 218
DB 61 DSSYELQVRAWPGSSYSGTWSWSDPVIPTOTSEELKEGWNPH 105

RESULT 14
US-08-780-562-7
Sequence 7, Application US/08/780562
Patent No. 6541604
GENERAL INFORMATION:
APPLICANT: Matthews, William
APPLICANT: Bennett, Brian
TITLE OF INVENTION: WSX RECEPTOR
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780,562
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585005
FILING DATE: 01/08/97
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/
FILING DATE: 01/08/97
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0986R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 783 amino acids
TYPE: Amino Acid
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TOPOLOGY: Linear
US-08-780-562-7

Query Match      12.1%; Score 144; DB 4; Length 783;
Best Local Similarity 31.1%; Pred. No. 6.5e-07;
Matches 57; Conservative 22; Mismatches 60; Indels 44; Gaps 11;

QY 39 LKDE---ATSCSLHRSANATHATYTCMDVFH-----FMADDIFSNTDQSGNYS 87
DB 177 LKDSFQVQCNSLRGC-----ECHVPVPRAKLYALIMYLEITTSAGVSFOSPLMS 227
QY 88 QEGGSFLLAESIKPAPP--FNVTVTFSGQYNISWSDYEDPAFYMLKGLQYELQYVNRG 145
DB 228 LQ--PMLV---VKPDPPLGLHREVTDDGNLKISWDSQTWAPP-----PLQYQVYLENS 276
QY 146 DPWAVSPRKLISVDSRSV-SLLPLEFRKDSSEYELQYVNRGPMGSSYSGTWSWSDPVI 204
DB 277 T--IVREAAEIVSATSLLDVSLP-----GSSYEYQVRSKRDLGS---GVWSDWSSPQVF 326
QY 205 QYQ 207
DB 327 TTQ 329

RESULT 15
US-08-599-455B-2
Sequence 2, Application US/08/599455B
Patent No. 5972621
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT
MODULATE BODY WEIGHT USING THE OB RECEPTOR
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,455B
FILING DATE: 22-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/017001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 894 amino acids
TYPE: amino acid
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Search completed: March 3, 2004, 12:39:55
Job time : 15.317 secs

GenCore version 5.1.6
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3M protein - protein search, using sw model

Run on: March 3, 2004, 12:25:04 ; Search time 8.19281 Seconds
(without alignments)

1385.519 Million cell updates/sec

Title: US-09-825-561A-6

Perfect score: 1195

Sequence: 1 CPDLVCYDYLTQVIGILEM.....SDPVIFQTQSEELKEGWNPH 218

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	1195	100.0	538	1 I21R HUMAN	Q9hbe5 homo sapien
2	844	70.6	529	1 I21R MOUSE	Q9jhx3 mus musculus
3	145	12.1	878	1 IL3B MOUSE	P26954 mus musculus
4	144	12.1	896	1 CYRB MOUSE	P26955 mus musculus
5	144	12.1	1162	1 LEPR MOUSE	P48356 mus musculus
6	141.5	11.8	539	1 IL2B MOUSE	P16297 mus musculus
7	139	11.6	635	1 TPOR HUMAN	P40238 homo sapien
8	138	11.5	1162	1 LEPR RAT	Q62959 rattus norv
9	137	11.5	1165	1 LEPR HUMAN	P48357 homo sapien
10	135.5	11.3	825	1 IL4R HUMAN	P24394 homo sapien
11	135	11.3	1163	1 LEPR MACMU	Q9mvl0 macaca mula
12	134	11.2	537	1 IL2B RAT	P26896 rattus norv
13	133.5	11.2	369	1 CYRG MOUSE	P34902 mus musculus
14	132.5	11.1	625	1 TPOR MOUSE	Q08351 mus musculus
15	129	10.8	1165	1 LEPR PIG	O02671 sus scrofa
16	127.5	10.7	379	1 CYRG BOVIN	Q95118 bos taurus
17	127	10.6	373	1 CYRG CANFA	P40321 canis famil
18	126	10.5	551	1 IL2B HUMAN	P14784 homo sapien
19	123	10.3	459	1 IL7R HUMAN	P16871 homo sapien
20	122	10.2	831	1 PRLR CHICK	Q04594 Gallus gall
21	121.5	10.2	918	1 IL6B RAT	P40190 rattus norv
22	120	10.0	369	1 CYRG HUMAN	P31785 homo sapien
23	118.5	9.9	862	1 IL2S HUMAN	Q99665 homo sapien
24	118	9.9	897	1 CYRB HUMAN	P32927 homo sapien
25	117	9.8	810	1 IL4R MOUSE	P16382 mus musculus
26	115.5	9.7	831	1 PRLR MELGA	Q91094 meleagris g
27	115	9.6	459	1 IL7R MOUSE	P16872 mus musculus
28	112.5	9.4	917	1 IL6B MOUSE	Q00560 mus musculus
29	110.5	9.2	918	1 IL6B HUMAN	P40189 homo sapien
30	108.5	9.1	638	1 IL6A HUMAN	P08887 homo sapien
31	106	8.9	468	1 GHR PIG	P19756 sus scrofa
32	105.5	8.8	460	1 IL6A MOUSE	P22272 mus musculus
33	105.5	8.8	638	1 GHR RAT	P16310 rattus norv

34	105	8.8	522	1 IL9R HUMAN	Q01113 homo sapien
35	104	8.7	638	1 GHR RABIT	P19941 oryctolagus
36	103	8.6	508	1 EPOR HUMAN	P19235 homo sapien
37	102	8.5	468	1 IL9R MOUSE	Q01114 mus musculus
38	99.5	8.3	467	1 IL6A PIG	O18796 sus scrofa
39	99.5	8.3	507	1 EPOR MOUSE	P14753 mus musculus
40	99	8.3	420	1 IL5R HUMAN	Q01344 homo sapien
41	97.5	8.2	662	1 IL2R HUMAN	P42701 homo sapien
42	97	8.1	462	1 IL6A RAT	P22273 rattus norv
43	95	7.9	415	1 IL5R MOUSE	P21183 mus musculus
44	95	7.9	581	1 PRLR CEREL	Q28235 cervus elap
45	94	7.9	328	1 IL2B MACMU	P48095 macaca mula

ALIGNMENTS

```

RESULT 1
ID I21R HUMAN STANDARD; PRT; 538 AA.
AC Q9HBE5; Q96HZ1; Q9HB91;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Interleukin 21 receptor precursor (IL-21R) (Novel interleukin
DE receptor).
GN IL21R OR NLR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20531754; PubMed=11081504;
RA Parrish-Novak J., Dillon S.R., Nelson A., Hammond A., Sprecher C.,
RA Gross J.A., Johnston J., Madden K., Xu W., West J., Schrader S.,
RA Burkhead S., Heipel M., Brandt C., Kuilper J.L., Kramer J.,
RA Conklin D., Presnell S.R., Berry J., Shiota F., Bort S., Hambly K.,
RA Mudri S., Clegg C., Moore M., Grant F.J., Lofton-Day C., Gilbert T.,
RA Raymond F., Ching A., Yao L., Smith D., Webster P., Whitmore T.,
RA Maurer M., Kaushansky K., Holly R.D., Foster D.;
RA "Interleukin 21 and its receptor are involved in NK cell expansion and
RA regulation of lymphocyte function.";
RL Nature 408:57-63(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20481926; PubMed=11016959;
RA Ozaki K., Kikly K., Michalovich D., Young P.R., Leonard W.J.;
RA "Cloning of a type I cytokine receptor most related to the IL-2
RA receptor beta chain.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:11439-11444(2000).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANTS CYS-191; ARG-318 AND SER-484.
RA Rieder M.J., Armet T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX TISSUE-B-cell, and Lymph;
RX MEDLINE=23285257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzly E.J., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kattaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

```

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.L., Skalska U., Smalusz D.B., Scherch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -!- FUNCTION: This is a receptor for interleukin-21.

CC -!- SUBUNIT: Heterodimer with the common gamma chain. Associates with JAK1.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- TISSUE SPECIFICITY: Selectively expressed in lymphoid tissues. Most highly expressed in thymus and spleen.

CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors. Subfamily 4.

CC -!- SIMILARITY: Contains 1 fibronectin type III domain.

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CC EMBL; AF254067; AAG9346.1; -

CC EMBL; AF269133; AAG23419.1; -

CC EMBL; AY064474; AAL39168.1; -

CC EMBL; BC004348; AAH04348.1; -

CC EMBL; BC007946; AAH07946.1; -

CC Genbank; HGNC:6006; IL21R.

CC MIM; 605383; C: integral to membrane; NAS.

CC GO; GO:0006021; C: integral to membrane; NAS.

CC GO; GO:0001533; F: interleukin-21 receptor activity; NAS.

CC GO; GO:0030101; P: natural killer cell activation; NAS.

CC InterPro; IPR003961; FN III.

CC InterPro; IPR003531; Hemoptoptn_S_F1.

CC SMART; SM00060; FN3; 1.

CC PROSITE; PS01355; HEMATOPO_REC_S_F1; FALSE_NEG.

KW Receptor; Transmembrane; Glycoprotein; Signal; Polymorphism.

FT SIGNAL 1 19 POTENTIAL.

FT CHAIN 20 538 INTERLEUKIN 21 RECEPTOR.

FT DOMAIN 20 232 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 233 253 POTENTIAL.

FT DOMAIN 254 538 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 120 209 FIBRONECTIN TYPE-III.

FT DISULFID 25 35 BY SIMILARITY.

FT DISULFID 65 81 POTENTIAL.

FT CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 125 125 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT VARIANT 131 191 R -> C (in dbSNP:3093370).

FT FTTC=VAR 014360.

FT S -> R (in dbSNP:3093385).

FT FTTC=VAR 014361.

FT G -> S (in dbSNP:3093386).

FT FTTC=VAR 014362.

FT AVP -> HEA (IN REF. 4; AAH07946).

FT G -> R (IN REF. 2).

SEQUENCE 538 AA; 59129 MW; 414079CCB974850A CRC64;

Query Match 100.0%; Score 1195; DB 1; Length 538;

Best Local Similarity 100.0%; Pred. No. 1.1e-96;

Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCYDYLQTVICILEMNLHSTLTWQDYELKDEATSCSLRAHNAATHATY 60

DB 20 CPDLVCYDYLQTVICILEMNLHSTLTWQDYELKDEATSCSLRAHNAATHATY 79

QY 61 TCHMDVFFHMADIFSVNITDQSGNYSCGSLAEISIKPAPPFNVTFTSGQYNISWR 120

Db 80 TCHMDVFFHMADIFSVNITDQSGNYSCGSLAEISIKPAPPFNVTFTSGQYNISWR 139

QY 121 SYEYPAPFMYLKGKLOYELQYRNGRDPWAVSPRKLISVDSESYLLPLEKDSYELQ 180

Db 140 SYEYPAPFMYLKGKLOYELQYRNGRDPWAVSPRKLISVDSESYLLPLEKDSYELQ 199

QY 181 VRAGMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218

Db 200 VRAGMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237

RESULT 2

ID 121R MOUSE STANDARD; PRT; 529 AA.

AC Q9JHX3; Q9BSML;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Interleukin 21 receptor precursor (IL-21R) (Novel interleukin DE receptor) (lymphocyte receptor beta) (LR-beta) (Novel cytokine DE receptor NR8).

GN IL21R OR NTLR.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI_taxid=10090;

OX [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6;

RC MEDLINE=20531754; PubMed=11081504;

RA Parrish-Novak J., Dillon S.R., Madden K., Xu W., West J., Schrader S., Burkhead S., Heipel M., Brandt C., Kuipjer J.L., Kramer J., Conklin D., Presnell S.R., Berry J., Grant F.J., Shiotani F., Bort S., Hamby K., Mudri S., Clegg C., Moore M., Grant F.J., Lofton-Day C., Gilbert T., Raymond F., Ching A., Yao L., Smith D., Webster P., Whitmore T., Maurer M., Kaushansky K., Holly R.D., Foster D.; "Interleukin 21 and its receptor are involved in NK cell expansion and regulation of lymphocyte function.";

RT Nature 408:57-63(2000).

RL [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Spleen, and Thymus;

RC MEDLINE=20481926; PubMed=11016959;

RA Ozaki K., Kikly K., Michalovich D., Young P.R., Leonard W.J.; "Cloning of a type I cytokine receptor most related to the IL-2 receptor beta chain.";

RT Proc. Natl. Acad. Sci. U.S.A. 97:11439-11444(2000).

RL [3]

RP SEQUENCE FROM N.A.

RA Donaldson D.D., Whitters M.J., Fitz L., Unger M., Finnerty H., Dagdigian C., Lowe L., Wood C.R., Young D.A., Collins M.; "Chromosome 16p12 encodes a biologically active IL-2Rb related receptor with lymphoid restricted expression.";

RT Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

RL [4]

RP SEQUENCE FROM N.A.

RC STRAIN=BALB/c;

RC Nomura H., Yaguchi N., Maeda M., Hasegawa M.; "A novel cytokine receptor NR8 is closely mapped to IL-4R.";

RT Polymorphism in Balb/c mouse.";

RT Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

RL [5]

RP SEQUENCE FROM N.A.

RC STRAIN=A/J, B10.S/DvTe, C57BL/6J, NOD/LtJ, and SJL/J; TISSUE=Spleen;

RA Gao J., Teuscher C.; "Mus musculus interleukin 21 receptor Gene IL21r mRNA.";

RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: This is a receptor for interleukin-21.

CC -!- SUBUNIT: Heterodimer with the common gamma chain. Associates with JAK1.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- TISSUE SPECIFICITY: Selectively expressed in lymphoid tissues.

CC Most highly expressed in thymus and spleen.
 CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
 CC Subfamily 4.
 CC -!- SIMILARITY: Contains 1 fibronectin type III domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AF254068; AAG23347.1; -
 CC EMBL; AF269134; AAG23420.1; -
 CC EMBL; AF279436; AAF86350.1; -
 CC EMBL; AB049137; BAB13736.1; -
 CC EMBL; AF477983; AAL82632.1; -
 CC EMBL; AF477983; AAL82633.1; -
 CC EMBL; AF477984; AAL82634.1; -
 CC EMBL; AF477985; AAL82635.1; -
 CC EMBL; AF477985; AAL82636.1; -
 CC MGD; MGI:1890475; IL21r.
 CC GO; GO:0004907; F:interleukin receptor activity; IDA.
 CC InterPro; IPR008957; FN.III-like.
 CC InterPro; IPR003961; FN.III.
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR007110; Ig-like.
 CC SMART; SM00060; FN3; 1.
 CC Receptor; Transmembrane; Glycoprotein; Signal; Polymorphism.
 CC PROSITE; PS01355; HEMATOPOREC_S_F1; FALSE NEG.
 CC SIGNAL 1 19
 CC CHAIN 19
 CC DOMAIN 20 237
 CC TRANSMEM 238 258
 CC DOMAIN 259 529
 CC DOMAIN 120 209
 CC DISULFID 25 35
 CC DISULFID 65 81
 CC CARBOHYD 73 73
 CC CARBOHYD 97 97
 CC CARBOHYD 104 104
 CC CARBOHYD 125 125
 CC CARBOHYD 182 182
 CC VARIANT 69 69
 CC VARIANT 200 200
 CC SEQUENCE 529 AA; 58354 MW; 8B41816B0D426581 CRC64;
 CC
 CC Query Match 70.6%; Score 844; DB 1; Length 529;
 CC Best Local Similarity 69.3%; Pred. No. 4.1e-66;
 CC Matches 151; Conservative 31; Mismatches 36; Indels 0; Gaps 0;
 CC
 CC 1 CPDLVCTDYLTQVTCILEMMNLHPSTLTWTQDQYBELKDEATSCSLHRSAAHATHATY 60
 CC 20 CLDLCTDYLTQVTCILEMMNLHPSTLTWTQDQYBELKDEATSCSLHRSAAHATHATY 79
 CC 61 TCHMDVFHMAADDIPSNIQTSGNYSQECGFLAIESIKPAPFNVTVPFGQYNISWR 120
 CC 80 TCHMPLSQFLSDEVFIVNTQSGNYSQECGFLAIESIKPAPFNVTVPFGQYNISWR 139
 CC 121 SDYEDPAFYMLKGLQYELQYVNRDGPVAVPRKLIISVDSRSVSLPLPEPRKDSSEYELQ 180
 CC 140 SAYDEPSNYVLGKQYELQYVNRDGPVAVPRKLIISVDSRSVSLPLPEPRKDSSEYELQ 199
 CC 181 VRAGPMPSGSSQGTWSEWSDPVIFQQTQSEELKEGNPH 218
 CC 200 VRAAPQPGTSPRGTWSEWSDPVIFQQTQSEELKEGNPH 237
 CC
 CC RESULT 3
 CC IL3B MOUSE
 CC ID IL3B MOUSE
 CC AC P26954;

DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Interleukin-3 receptor class II beta chain precursor (Colony
 DE stimulating factor 2 receptor, beta 2 chain).
 GN CSF2RB2 OR AI2CA OR IL3RB2 OR IL3R.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90117145; PubMed=2404337;
 RA Itoh N., Yonehara S., Schreurs J., Gorman D.M., Maruyama K., Ishii A.,
 RA Yanara I., Arai K., Miyajima A.;
 RT "Cloning of an interleukin-3 receptor gene: a member of a distinct
 RT receptor gene family.";
 RL Science 247:324-327(1990).
 CC -!- FUNCTION: In mouse, there are two classes of high-affinity IL3
 CC receptors. One contains this IL3-specific beta chain and the other
 CC contains the beta chain also shared by high-affinity IL5 and GM-
 CC CSF receptors.
 CC -!- SUBUNIT: Heterodimer of an alpha and a beta chain.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
 CC Subfamily 4.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; M29855; AAA32955.1; -
 CC PIR; A40091; A40091.
 CC MGD; MGI:1339760; Csf2rb2.
 CC InterPro; IPR002996; CRIA.
 CC InterPro; IPR00282; Cytok_receptor_2.
 CC InterPro; IPR008957; FN.III-like.
 CC InterPro; IPR003961; FN.III.
 CC InterPro; IPR003531; Hemtopoptn_S_F1.
 CC Pfam; PF00041; fn3; 2.
 CC SMART; SM00060; FN3; 2.
 CC PROSITE; PS01355; HEMATOPOREC_S_F1; 1.
 CC Receptor; Transmembrane; Glycoprotein; Signal.
 CC SIGNAL 1 22
 CC CHAIN 23 878
 CC DOMAIN 23 440
 CC TRANSMEM 441 462
 CC DOMAIN 463 878
 CC DISULFID 39 49
 CC DISULFID 78 95
 CC DISULFID 254 264
 CC DISULFID 293 310
 CC CARBOHYD 350 350
 CC SEQUENCE 878 AA; 97195 MW; 8BEC9092ADC24D56 CRC64;
 CC
 CC Query Match 12.1%; Score 145; DB 1; Length 878;
 CC Best Local Similarity 23.0%; Pred. No. 6.2e-05;
 CC Matches 48; Conservative 38; Mismatches 97; Indels 26; Gaps 7;
 CC
 CC 3 DLVCTDYLTQVTCILEMMNLHPSTLTWTQDQYBELKDEATSCSLHRSAAHATHATY 62
 CC 251 NLQCFDGIQSLHCSWEVNTQTGVSFGLFVRPSAPAEKSPVKEPQASVVVTRVC 310
 CC 63 HMDVFHMAADDIPSNIQTSGNYSQECGFLAIESIKPAPFNVTVPFGQYNISWR 121
 CC 311 SLVPEPSAHSQITVSX-----HLEQKFTMSYTHIQMEPPIILNQTNRDVSLSHWET 364

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QY 122 D-----YEDAFYMLKGLQYELQYENRGDPWAVSPRKLISVDSRSVSLPLPFRKDSY 177
DB 365 QXIPYIDHTF-----QYCKKESKWSKXTENLGRVNSMD---LP-QLEPDTISY 411

QY 178 ELQVRAGMPGSSYQGTWSEWSDPVIFOT 206
DB 412 CARVRVKPI--SDYGIWSEWSENYTWT 438

RESULT 4
CYRB MOUSE
ID CYRB MOUSE STANDARD; PRT; 896 AA.
AC P26955;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cytokine receptor common beta chain precursor (CDw131 antigen) (GM-
DE CSF1L3/IL-5 receptor common beta chain).
GN CSF2RB OR CSF2RB1 OR AIC2B OR IL3RB1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90319131; PubMed=1695379;
RA Gorman D.M., Itoh N., Kitamura T., Schreurs J., Yorehara S.,
RA Yahara I., Arai K., Miyajima A.;
RT "Cloning and expression of a gene encoding an interleukin 3 receptor-
RT like protein: identification of another member of the cytokine
RT receptor gene family";
RL Proc. Natl. Acad. Sci. U.S.A. 87:5459-5463(1990).
CC -!- FUNCTION: High affinity receptor for interleukin-3, interleukin-5
CC and granulocyte-macrophage colony-stimulating factor.
CC -!- SUBUNIT: Heterodimer of an alpha and a beta chain. The beta chain
CC is common to the IL3, IL5 and GM-CSF receptors.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC Subfamily 4.
CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announcement/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M34397; AAA37204.1; -
DR F1R; A35782; A35782
DR MGD; MGI:1339759; Csf2rb1.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR000282; Cytok_receptor_2.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003961; FN_III.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS01355; HEWATOPO_REC_S_F1; 1. Repeat; Signal.
KW Receptor; transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 22
FT CHAIN 23 896 CYTOKINE RECEPTOR COMMON BETA CHAIN.
FT DOMAIN 23 441 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 442 463 POTENTIAL.
FT DOMAIN 464 896 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 132 241 FIBRONECTIN TYPE-III 1.
FT DOMAIN 343 440 FIBRONECTIN TYPE-III 2.
FT DISULFID 39 49 BY SIMILARITY.
FT DISULFID 77 99 BY SIMILARITY.
FT DISULFID 88 94 BY SIMILARITY.
FT DISULFID 253 263 BY SIMILARITY.
FT DISULFID 292 310 BY SIMILARITY.
FT CARBOHYD 62 62 N-LINKED (GLCNAC...) (POTENTIAL).

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FT CARBOHYD 141 141 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 350 350 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 896 AA; 99111 MW; 8C16EDFDC07A999 CRC64;

Query Match 12.1%; Score 144; DB 1; Length 896;
Best Local Similarity 22.6%; Pred. No. 7.7e-05;
Matches 49; Conservative 41; Mismatches 87; Indels 40; Gaps 9;

QY 3 DLVCYTDYLQTVICILEMWN-----LHPSTLTITWQDYELKDBATSCSLHRS 51
DB 250 NLQCFDGIQSLHCSWEVWVTTQTSVSGLFTRPSVA-----PEKCSPVKEP 299
QY 52 AHNATHATYTCMDVDFHFMADIFSVNITDQSGNYSQEGSFLLA-ESIKPAPP-FNVTV 109
DB 300 PGASVVTYRVCYSLPVPPESAHQYTVSVK-----HLEQKFKIMSNNHQMPEPTLNLT 353
QY 110 TFSQYQNIWRSRDYEDPAPYMLKGLQYELQYENRGDPWAVSPRKLISVDSRSVSLPL 169
DB 354 N-RDSYSLHWETQKWAYSFI-----EHTFOVQYKKSKSDSWEDSKTENLDRAHSM 404
QY 170 EFRKDSYELQVRAGMPGSSYQGTWSEWSDPVIFOT 206
DB 405 QLEPDTISYCARVRVKPI--SNYDGIWSEWSENYTWT 439

RESULT 5
LEPR MOUSE
ID LEPR MOUSE STANDARD; PRT; 1162 AA.
AC P48356; O35686; O54986; Q61215; Q64309; Q9QWV5;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Leptin receptor precursor (LEP-R) (OB receptor) (OB-R) (B219).
GN LEPR OR OBR OR DB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM A).
RX TISSUE=Choroid plexus;
RX MEDLINE=96128129; PubMed=8548812;
RA Tartaglia L.A., Dembski M., Weng X., Deng N., Culpepper J.,
RA Davos R., Richards G.J., Campfield L.A., Clark P.T., Deeds J.,
RA Muir C., Sanker S., Moriarty A., Moore K.J., Smutko J.S.,
RA Mays G.G., Woolf E.A., Monroe C.A., Tepper R.I.;
RT "Identification and expression cloning of a leptin receptor, OB-R.";
RT Cell 83:1263-1271(1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM B).
RX STRAIN=C57BL/KsJ; TISSUE=Hypothalamus;
RX MEDLINE=96190816; PubMed=8608603;
RA Chen H., Charlat O., Tartaglia L.A., Woolf E.A., Weng X.,
RA Ellis S.J., Lakey N.D., Culpepper J., Moore K.J., Breitbart R.E.,
RA Duyk G.M., Tepper R.I., Morgenstern J.P.;
RT "Evidence that the diabetes gene encodes the leptin receptor:
RT identification of a mutation in the leptin receptor gene in db/db
RT mice.";
RL Cell 84:491-495(1996).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS A; B; C; D AND E).
RX STRAIN=C57BL/KsJ; TISSUE=Hypothalamus;
RX MEDLINE=96231937; PubMed=8628397;
RA Lee G.-H., Froenca R., Montez J.M., Carroll K.M., Darvishzadeh J.G.,
RA Lee J.I., Friedman J.M.;
RT "Abnormal splicing of the leptin receptor in diabetic mice.";
RL Nature 379:632-635(1996).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM C).
RX STRAIN=BALB/c; TISSUE=Liver;
RX MEDLINE=96206286; PubMed=8616721;
RA Cioffi J.A., Shafer A.W., Zupancic T.J., Smith-Gbur J.,
RA Mikhail A., Platika D., Snodgrass H.R.;

```


RT "Novel B219/OB receptor isoforms: possible role of leptin in
XT hematoopoiesis and reproduction.";
XL Nat. Med. 2:585-589(1996).
[5]
RN SEQUENCE FROM N.A. (ISOFORM B).
RP STRAIN=NZO; TISSUE=Hypothalamus;
RC MEDLINE=97462708; PubMed=9322935;
RZ Igel M., Becker W., Herberg L., Joest H.G.;
RA "Hyperleptinemia, leptin resistance, and polymorphic leptin receptor
XT in the New Zealand obese mouse.";
YL Endocrinology 138:4234-4239(1997).
[6]
RN SEQUENCE FROM N.A. (ISOFORMS A AND B).
RP STRAIN=FVB/N; TISSUE=Spleen;
RC MEDLINE=96270520; PubMed=8692797;
RZ Ghilardi N., Ziegler S., Wiestner A., Stoffel R., Heim M.H.,
RA Skoda R.C.;
XT "Defective STAT signaling by the leptin receptor in diabetic mice.";
YL Proc. Natl. Acad. Sci. U.S.A. 93:6231-6235(1996).
[7]
RN SEQUENCE FROM N.A. (ISOFORMS A; B; C AND E).
RP STRAIN=129/J;
RC MEDLINE=98008913; PubMed=9344648;
RZ Chua S.C., Koutlas I.K., Han L., Liu S.M., Kay J., Young S.J.,
RA Chung W.K., Leibell R.L.;
XT "Fine structure of the murine leptin receptor gene: splice site
YT suppression is required to form two alternatively spliced
YL transcripts.";
RN Genomics 45:264-270(1997).
[8]
RN SEQUENCE FROM N.A. (ISOFORM B), AND VARIANT ASN-600.
RP STRAIN=KK Obese; TISSUE=Hypothalamus;
RC MEDLINE=99061814; PubMed=9845674;
RZ Igel M., Taylor B.A., Phillips S.J., Becker W., Herberg L.,
RA Joest H.G.;
XT "Hyperleptinemia and leptin receptor variant Asp600Asn in the obese,
YT hyperinsulinemic KK mouse strain.";
YL J. Endocrinol. 21:337-345(1998).
[9]
RN SEQUENCE OF 890-1162 FROM N.A. (ISOFORM B).
RP STRAIN=129;
RC STRAIN=A.S., Myers M.G. Jr.;
RZ "Murine leptin receptor genomic exon 18b and surrounding sequence.";
RA Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
[10]
RN PHOSPHORYLATION OF TYR-985 AND TYR-1138, AND MUTAGENESIS OF TYR-985;
RP TYR-1077 AND TYR-1138.
RZ MEDLINE=20261588; PubMed=10799542;
RA Banks A.S., Davis S.M., Bates S.H., Myers M.G. Jr.;
XT "Activation of downstream signals by the long form of the leptin
YT receptor.";
YL J. Biol. Chem. 275:14563-14572(2000).
[11]
RN - FUNCTION: The short form (isoform A) may act to transport leptin
XT to the cerebrospinal fluid. The putative soluble receptor (isoform
YL E) could function as a transport protein.
[12]
RN - SUBCELLULAR LOCATION: Type I membrane protein. Except for form E
XT which could be secreted.
[13]
RN - ALTERNATIVE PRODUCTS:
XT Event=Alternative splicing; Named isoforms=5;
YL Name=B;
[14]
RN IsoId=P49356-1; Sequence=Displayed;
XT Name=A;
YL IsoId=P49356-2; Sequence=VSP_001697, VSP_001698;
[15]
RN Name=C;
YL IsoId=P49356-3; Sequence=VSP_001699, VSP_001700;
[16]
RN Name=D;
YL IsoId=P49356-4; Sequence=VSP_001701, VSP_001702;
[17]
RN Name=E;
YL IsoId=P49356-5; Sequence=VSP_001703, VSP_001704;
[18]
RN - TISSUE SPECIFICITY: Isoform A: highest level of expression in lung
XT and kidney, also present in kidney, heart, brain, spleen, liver,
YL muscle, choroid plexus and hypothalamus. Isoform B: highest level
[19]
RN of expression in hypothalamus and lower level in brain, testes and
YL adipose tissue. Isoform E: expressed in adipose tissue,
[20]
RN hypothalamus, heart, and testes.
[21]
RN - PTM: Phosphorylated on two tyrosine residues. Tyr-985 may be the
XT major site of phosphorylation. Phosphorylation on both sites is
YL required for full activity.
[22]
RN - SIMILARITY: Belongs to the type I cytokine family of receptors.
[23]
RN Subfamily 2.
[24]
RN - SIMILARITY: Contains 3 fibronectin type III domains.
[25]
RN - SIMILARITY: Contains 1 immunoglobulin-like domain.
[26]
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RN or send an email to license@isb-sib.ch).
[29]
RN -----
[30]
RN EMBL; U42467; AAC93014.1; -
DR EMBL; U46135; AAC52408.1; -
DR EMBL; U49106; AAC52420.1; -
DR EMBL; U49107; AAC52421.1; -
DR EMBL; U49108; AAC52422.1; -
DR EMBL; U49109; AAC52423.1; -
DR EMBL; U49110; AAC52424.1; -
DR EMBL; U52915; AAC52599.1; -
DR EMBL; Y10298; CAA71343.1; -
DR EMBL; U58861; AAC52705.1; -
DR EMBL; U58862; AAC52706.1; -
DR EMBL; U58863; AAC52707.1; -
DR EMBL; AF039456; AAB95334.1; -
DR EMBL; AF039443; AAB95334.1; JOINED.
DR EMBL; AF039444; AAB95334.1; JOINED.
DR EMBL; AF039445; AAB95334.1; JOINED.
DR EMBL; AF039446; AAB95334.1; JOINED.
DR EMBL; AF039447; AAB95334.1; JOINED.
DR EMBL; AF039448; AAB95334.1; JOINED.
DR EMBL; AF039449; AAB95334.1; JOINED.
DR EMBL; AF039450; AAB95334.1; JOINED.
DR EMBL; AF039451; AAB95334.1; JOINED.
DR EMBL; AF039452; AAB95334.1; JOINED.
DR EMBL; AF039453; AAB95334.1; JOINED.
DR EMBL; AF039454; AAB95334.1; JOINED.
DR EMBL; AF039455; AAB95334.1; JOINED.
DR EMBL; AF039461; AAB95333.1; ALT TERM.
DR EMBL; AF039463; AAB95333.1; JOINED.
DR EMBL; AF039444; AAB95333.1; JOINED.
DR EMBL; AF039445; AAB95333.1; JOINED.
DR EMBL; AF039446; AAB95333.1; JOINED.
DR EMBL; AF039447; AAB95333.1; JOINED.
DR EMBL; AF039448; AAB95333.1; JOINED.
DR EMBL; AF039449; AAB95333.1; JOINED.
DR EMBL; AF039450; AAB95333.1; JOINED.
DR EMBL; AF039451; AAB95333.1; JOINED.
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DR EMBL; AF039455; AAB95333.1; JOINED.
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DR EMBL; AF039457; AAB95333.1; JOINED.
DR EMBL; AF039458; AAB95333.1; JOINED.
DR EMBL; AF039459; AAB95333.1; JOINED.
DR EMBL; AF039459; AAB95335.1; -
DR EMBL; AF039443; AAB95335.1; JOINED.
DR EMBL; AF039444; AAB95335.1; JOINED.
DR EMBL; AF039445; AAB95335.1; JOINED.
DR EMBL; AF039446; AAB95335.1; JOINED.
DR EMBL; AF039447; AAB95335.1; JOINED.
DR EMBL; AF039448; AAB95335.1; JOINED.

DR EMBL; AF039449; AAB95335.1; JOINED.
 DR EMBL; AF039450; AAB95335.1; JOINED.
 DR EMBL; AF039451; AAB95335.1; JOINED.
 DR EMBL; AF039452; AAB95335.1; JOINED.
 DR EMBL; AF039453; AAB95335.1; JOINED.
 DR EMBL; AF039454; AAB95335.1; JOINED.
 DR EMBL; AF039455; AAB95335.1; JOINED.
 DR EMBL; AF039456; AAB95335.1; JOINED.

Query Match 12.1%; Score 144; DB 1; Length 1162;
 Best Local Similarity 31.1%; Pred. No. 0.00011;
 Matches 57; Conservative 22; Mismatches 60; Indels 44; Gaps 11;

QY 39 LKDE-----ATSCSLHRSAAHATHATYTCHEMDFH-----FMADDIFSNNITDQSGNYS 87
 DB 177 LKDSFQTCNCLRG-----ECHVFPRAKNYALLWLEITSAGVSFQSLMS 227
 QY 88 QECGSLAEISIKPAPP--FNVVTFSCQYNISWSDYEDPAFVLMKGKQYELQYRNRG 145
 DB 228 LQ--PMLV---VKPDPPGLHMEVTDGDKLSWDSQTMAPP-----PLQYQVKYLENS 276
 QY 146 DPWAYSPRKLIISVDSRSV-SLLPLFRKDSYELQVRAGMPGSSYQGTWSEMSDPVIF 204
 DB 277 T--IVREAARIVSATSLIVDSVLP-----GSSYEVQVRSKELDGS---GYWSDWSSPQVF 326
 QY 205 QTK 207
 DB 327 TTQ 329

RESULT 6
 IL2B_MOUSE
 ID IL2B_MOUSE STANDARD; PRT; 539 AA.
 AC P16297;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Interleukin-2 receptor beta chain precursor (IL-2 receptor) (P70-75)
 DE (High affinity IL-2 receptor beta subunit) (CD122).
 GN IL2RB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90175385; PubMed=2155425;
 RA Kono T., Doi T., Yamada G., Hatakeyama M., Minamoto S., Tsudo M.,
 RA Miyasaka M., Miyata T., Taniguchi T.;
 RT "Murine interleukin 2 receptor beta chain: dysregulated gene
 expression in lymphoma line EL-4 caused by a promoter insertion.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:1806-1810(1990).
 CC -!- FUNCTION: Receptor for interleukin 2. This beta subunit is
 CC involved in receptor mediated endocytosis and transduces the
 CC mitogenic signals of IL2.
 CC -!- SUBUNIT: Noncovalent dimer of an alpha and a beta chains. IL2R
 CC exists in 3 different forms: a high affinity dimer, an
 CC intermediate affinity monomer (beta chain), and a low affinity
 CC monomer (alpha chain). The high and intermediate affinity forms
 CC also associate with a gamma chain.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
 CC Subfamily 4.

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 or send an email to license@isb-sib.ch).

DR EMBL; M28052; AAA39283.1; -.

DR PIR; A35052; A35052.
 DR HSSP; P14784; IILM.
 DR MGD; MGI:98550; I12rb.
 DR InterPro; IPR002996; CRIA.
 DR InterPro; IPR008957; FN.III-like.
 DR InterPro; IPR003961; FN.III.
 DR InterPro; IPR003531; Hemtopoptn_S_F1.
 DR Pfam; PF00041; fn3.1.
 DR SMART; SM0060; FN3.1.
 DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
 KW Receptor; transmembrane; Glycoprotein; Signal.
 FT CHAIN 27 539 INTERLEUKIN-2 RECEPTOR BETA CHAIN.
 FT SIGNAL 1 26 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 27 240 POTENTIAL.
 FT TRANSMEM 241 268 POTENTIAL.
 FT DOMAIN 269 539 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 36 46 BY SIMILARITY.
 FT DISULFID 74 86 BY SIMILARITY.
 FT CARBOHYD 30 30 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 43 43 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 55 55 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 71 71 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 150 150 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 216 216 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 539 AA; 60538 MW; 365C9D20E86FE14 CRC64;

Query Match 11.8%; Score 141.5; DB 1; Length 539;
 Best Local Similarity 22.5%; Pred. No. 6.8e-05;
 Matches 54; Conservative 43; Mismatches 86; Indels 57; Gaps 12;

QY 1 CPDLVCTDYLTQVICILEMNLHPSLTLTWTQDQYELKDEATSCSLHRSAAHATHATY 60
 DB 31 CSHLECFYNSRANVSC---MWS-HEEALNV-----TTCVHAKS-NLRHWNK 72
 QY 61 TCHMDVFH-----FMADDIFSNNIT--DQSGNYSQECGSLAEISIK 100
 DB 73 TCELTIVRQASWACNLILGSPFSSQSLTSVLLDINVCWEKGRVVKTCDFHFDNLR 132
 QY 101 PAPPENVTYTF--SQYINISW---SDYEPAPFVLMKGKQYELQYRNRPVSPRR 154
 DB 133 LVAPSLQVLIHIDTORCNISWKSQVSHYIF-----YLFERRLLGSHWEDA--- 182
 QY 155 KLISVDSRSVSLPLLEFRKDSYELQVRAGMPGSSYQGTWSEMSDPVIFOTQ-SEELKE 213
 DB 183 SVLSLKQKQVQLFLEMLIPSTSYEVQVRSKELDGS---GTWSPNSQPLTFRTRPADPMKE 240

RESULT 7
 TPOR_HUMAN
 ID TPOR_HUMAN STANDARD; PRT; 635 AA.
 AC P40238;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Thrombopoietin receptor precursor (TPO-R) (Myeloproliferative leukemia
 DE protein) (C-mpl) (CD110 antigen).
 GN MPL OR TPOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RX MEDLINE=92302297; PubMed=1608974;
 RA Vigon I., Mornon J.-P., Cocault L., Mitjavila M.-T., Tambourin P.,
 RA Gisselbrecht S., Souvri M.;
 RT "Molecular cloning and characterization of MPL, the human homolog of
 RT the v-mpl oncogene: identification of a member of the hematopoietic
 RT growth factor receptor superfamily";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:5640-5644(1992).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RX MEDLINE=94292186; PubMed=8020956;

RA Mignotte V., Vigon I., Boucher de Crevecoeur E., Romeo P.-H.,
RA Lemarchandel V., Chretien S.;
RT "Structure and transcription of the human c-mpl gene (MPL).";
RL Genomics 20:5-12(1994).
RN [3]
RP VARIANTS VAL-58 AND LYS-168.
RX MEDLINE=9318093; PubMed=10391209;
RA Cargill M., Althuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
RA Friedland L., Rolf E.P., Kalyanaram N., Nemesh J., Ziaugra L.,
RA Friedland L., Rolf E., Warrington J., Lipshutz R., Daley G.Q.,
RA Lander E.S.;
RT "Characterization of single-nucleotide polymorphisms in coding regions
of human genes.";
RL Nat. Genet. 22:231-238(1999).
RN [4]
RP ERRATUM.
RA Cargill M., Althuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
RA Shaw N., Lane C.R., Lim E.P., Kalyanaram N., Nemesh J., Ziaugra L.,
RA Friedland L., Rolf E., Warrington J., Lipshutz R., Daley G.Q.,
RA Lander E.S.;
RL Nat. Genet. 23:373-373(1999).
CC -!- FUNCTION: Receptor for thrombopoietin. May represent a regulatory
molecule specific for TPO-R-dependent immune responses.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=C-mpl-P;
CC IsoId=P40238-1; Sequence=Displayed;
CC Name=2; Synonyms=C-mpl-K;
CC IsoId=P40238-2; Sequence=VSP 001734, VSP 001735;
CC -!- TISSUE SPECIFICITY: Expressed at a low level in a large number of
cells of hematopoietic origin. The two isoforms are always found
to be coexpressed.
CC -!- DISEASE: Defects in MPL are a cause of congenital anegakaryocytic
thrombocytopenia (CAMT) [MIM:604498]. CAMT is a disease
characterized by isolated thrombocytopenia and megakaryocytopenia
with no physical anomalies.
CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC Subfamily 1.
CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC -!- CAUTION: It is uncertain whether Met-1 or Met-8 is the initiator.
CC -!- DATABASE: NAME=PROW; NOTE=PROW 1:22-25(2000);
CC WWW="http://www.ncbi.nlm.nih.gov/prow/guide/11586825_g.htm".
CC -----
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M90102; AAA639971.1; -;
DR EMBL; M90103; AAA639972.1; -;
DR EMBL; U68162; AAB08424.1; -;
DR EMBL; U68159; AAB08424.1; JOINED.
DR EMBL; U68160; AAB08424.1; JOINED.
DR EMBL; U68161; AAB08424.1; JOINED.
DR EMBL; U68162; AAB08425.1; -;
DR EMBL; U68159; AAB08425.1; JOINED.
DR EMBL; U68160; AAB08425.1; JOINED.
DR EMBL; U68161; AAB08425.1; JOINED.
DR EMBL; U68162; AAB08425.1; JOINED.
DR PIR; A45266; A45266.
DR PIR; B45266; B45266.
DR HSPSP; P12335; 1EBA.
DR Genew; HGNC:7217; MPL.
DR MIM; 159530; -;
DR MIM; 604498; -;
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0004888; F:transmembrane receptor activity; TAS.
DR GO; GO:0008283; P:cell proliferation; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
DR InterPro; IPR002996; CR1A.

DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003528; Hemtopoptn_L_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS01352; HEMATOPO REC L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing;
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 635 THROMBOPOIETIN RECEPTOR.
FT DOMAIN 26 491 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 492 513 POTENTIAL.
FT DOMAIN 514 635 CYTOPLASMIC (POTENTIAL).
FT DISULFID 40 50 BY SIMILARITY.
FT DISULFID 77 93 BY SIMILARITY.
FT DISULFID 291 301 BY SIMILARITY.
FT DISULFID 323 334 BY SIMILARITY.
FT CARBOHYD 117 117 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 178 178 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 298 298 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 358 358 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARSPPLIC 523 579 RLRHALWPSLDLHRLVGLGYLDTAALSPPKATVSDTCEEV
EPSLLEILPKSSERTP -> YRPROAGDWRTWRSRTCKQA
FLVRSVTDLRPPPTVRYTGFALPARHLWDSPRLTL (in
isoform 2).
FT VARSPPLIC 580 635 /FTid=VSP_001734.
FT VARIANT 58 58 Missing (in isoform 2).
FT VARIANT 58 58 A -> V (in dbSNP:6087).
FT VARIANT 168 168 /FTid=VAR_011988.
FT VARIANT 168 168 E -> K (in dbSNP:6088).
FT VARIANT 168 168 /FTid=VAR_011989.
SQ SEQUENCE 635 AA; 71244 MW; D25D8D859359DDC CRC64;
Query Match 11.6%; Score 139; DB 1; Length 635;
Best Local Similarity 24.0%; Pred. No. 0.00014;
Matches 59; Conservative 25; Mismatches 76; Indels 86; Gaps 14;
QY 4 LVCTDYDTQVICILEMNLHPSLTITWQDYBELKDEATCSL--HRSAHNATHATY- 60
DB 289 LQCFTLDLKNVTC-----QWQQ-----DHASSQGFYHSHRACCPDRYP 329
QY 61 -----TCHM-----DVHFMADDIFSVNITDSGNYSECSS-F 93
DB 330 IWNECEEKNTNGLQTPQFRCFKGRNDSIIHL-----VEVTAPGVTHYLSGPF 383
QY 94 LIAESIK-PAPPFNVTTFSGQYNISWRSDYEDPAFYMLKGLQYELQYRNRG-DPWAVS 151
DB 384 WTHQAVRLPTNLHWRLEISSGHLEW-----QHFSSWAAQ-ETCYQLRYTGEGHDKV- 437
QY 152 PARKLISVDSRSVLLP-----LEFRKDSYELQVRAGPMGSSYQGTWSEWSDPI 203
DB 438 -----LEPLLGARGGTLELRPSRYLQIRA-RINGPTYQGFWSSWDPT 482
QY 204 FOTQSE 209
DB 483 VETATE 488
RESULT 8
LEPR RAT
ID LEPR RAT STANDARD; PRT; 1162 AA.
AC Q62959; Q35772; Q54805; P70493; P70494; P70495; P97589;
AC Q62960; Q63007; Q63385; Q63386; Q9ER14;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Leptin receptor precursor (LEP-R) (OB receptor) (OB-R).
GN LEPR OR OBR OR FA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;

[1] SEQUENCE FROM N.A. (ISOFORM B), AND VARIANT FA PRO-269.
 RP STRAIN=Zucker; TISSUE=Hypothalamus;
 RX MEDLINE=96241565; PubMed=8673096;
 RA Phillips M.S., Liu Q., Hammond H.A., Dugan V., Hey P.J., Caskey C.T.,
 RA Hess J.F.,
 RT "Leptin receptor missense mutation in the fatty Zucker rat.";
 RL Nat. Genet. 13:18-19(1996).
 [2] SEQUENCE FROM N.A. (ISOFORM B), AND VARIANT FA PRO-269.
 RP STRAIN=Sprague-Dawley, and Zucker fatty; TISSUE=Brain;
 RX MEDLINE=96295531; PubMed=8702432;
 RA Iida M., Murakami T., Ishida K., Mizuno A., Kuwajima M., Shima K.;
 RT "Substitution at codon 269 (Glutamine --> proline) of the leptin
 RT receptor (OB-R) cDNA is the only mutation found in the Zucker fatty
 RT (fa/fa) rat.";
 RL Biochem. Biophys. Res. Commun. 224:597-604(1996).
 [3] SEQUENCE FROM N.A. (ISOFORMS A; B AND E), AND VARIANT FA PRO-269.
 RP STRAIN=Sprague-Dawley, and Zucker fatty;
 RX MEDLINE=96332408; PubMed=8769097;
 RA Takaya K., Ogawa Y., Isse N., Okazaki T., Satoh N., Masuzaki H.,
 RA Mori K., Tamura N., Hosoda K., Nakao K.;
 RT "Molecular cloning of rat leptin receptor isoform complementary
 RT DNAs -- identification of a missense mutation in Zucker fatty (fa/fa)
 RT rats.";
 RL Biochem. Biophys. Res. Commun. 225:75-83(1996).
 [4] SEQUENCE FROM N.A. (ISOFORM B).
 RP STRAIN=Sprague-Dawley, and Zucker fatty;
 RX MEDLINE=96212906; PubMed=8630068;
 RA Iida M., Murakami T., Ishida K., Mizuno A., Kuwajima M., Shima K.;
 RT "Phenotype-linked amino acid alteration in leptin receptor cDNA from
 RT Zucker fatty (fa/fa) rat.";
 RL Biochem. Biophys. Res. Commun. 222:19-26(1996).
 [5] SEQUENCE FROM N.A. (ISOFORM B).
 RP STRAIN=Sprague-Dawley, and Zucker fatty;
 RX MEDLINE=96212906; PubMed=8630068;
 RA Iida M., Murakami T., Ishida K., Mizuno A., Kuwajima M., Shima K.;
 RT "Phenotype-linked amino acid alteration in leptin receptor cDNA from
 RT Zucker fatty (fa/fa) rat.";
 RL Biochem. Biophys. Res. Commun. 222:19-26(1996).
 [6] SEQUENCE FROM N.A. (ISOFORM B).
 RP STRAIN=Sprague-Dawley; TISSUE=Spleen;
 RX MEDLINE=96368027; PubMed=8772180;
 RA Park J.H., Ju S.K., Na S.Y., You K.H., Kim K.L.;
 RT "Molecular cloning, sequencing, and recombinant expression of the long
 RT form of the rat leptin receptor isolated from whole spleen RNA.";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 [7] SEQUENCE FROM N.A. (ISOFORM F).
 RP STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=96368027; PubMed=8772180;
 RA Wang M.-Y., Zhou Y.T., Newgard C.B., Unger R.H.;
 RT "A novel leptin receptor isoform in rat.";
 RL FEBS Lett. 392:87-90(1996).
 [8] SEQUENCE OF 1-123 FROM N.A.
 RP MORISHITA T., HIGAKI T., KUZUYAMA T., NOGUCHI T.;
 RT "Analysis of rat leptin receptor gene.";
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 [9] SEQUENCE OF 557-802 AND 843-892 FROM N.A. (ISOFORMS C AND E).
 RP STRAIN=Sprague-Dawley;
 RX MEDLINE=97415825; PubMed=9268737;
 RA Chien E.K., Hara M., Rouard M., Yaro H., Phillippe M., Polonsky K.S.,
 RA Bell G.I.;
 RT "Increase in serum leptin and uterine leptin receptor messenger RNA
 RT levels during pregnancy in rats.";
 RL Biochem. Biophys. Res. Commun. 237:476-480(1997).
 [10] SEQUENCE OF 694-878 FROM N.A.
 RP STRAIN=Sprague-Dawley; TISSUE=Pancreas;
 RX MEDLINE=97415825; PubMed=9268737;
 RA Chien E.K., Hara M., Rouard M., Yaro H., Phillippe M., Polonsky K.S.,
 RA Bell G.I.;

"Identification of a leptin receptor in islet.";
 Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
 [11] SEQUENCE OF 821-894 FROM N.A. (ISOFORM A).
 RP STRAIN=Wistar Munich; TISSUE=Kidney;
 RX MEDLINE=96314329; PubMed=8690163;
 RA Chua S.C. Jr., White D.W., Wu-Peng X.S., Liu S.M., Okada N.,
 RA Kerslaw E.B., Chung W.K., Power-McKee L., Chua M., Tartaglia L.A.,
 RA Leibel R.L.;
 RT "Phenotype of fatty due to Gln269Pro mutation in the leptin receptor
 RT (lepr).";
 RL Diabetes 45:1141-1143(1996).
 [12] VARIANT FA PRO-269.
 RP MEDLINE=96314329; PubMed=8690163;
 RX Chua S.C. Jr., White D.W., Wu-Peng X.S., Liu S.M., Okada N.,
 RA Kerslaw E.B., Chung W.K., Power-McKee L., Chua M., Tartaglia L.A.,
 RA Leibel R.L.;
 RT "Phenotype of fatty due to Gln269Pro mutation in the leptin receptor
 RT (lepr).";
 RL Diabetes 45:1141-1143(1996).
 CC -!- FUNCTION: Receptor for obesity factor (leptin). Involved in the
 CC regulation of fat metabolism and in a hematopoietic pathway
 CC required for normal lymphopoiesis. May play a role in
 CC reproduction.
 CC -!- FUNCTION: The short form (isoform A) may act to transport leptin
 CC to the cerebrospinal fluid. The putative soluble receptor (isoform
 CC B) could function as a transport protein.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Except for form E
 CC which could be secreted.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=6;
 CC Name=B;
 CC IsoId=Q62959-1; Sequence=Displayed;
 CC Name=A;
 CC IsoId=Q62959-2; Sequence=VSP_001705, VSP_001706;
 CC Name=C;
 CC IsoId=Q62959-3; Sequence=VSP_001707, VSP_001708;
 CC Name=D;
 CC IsoId=Q62959-6; Sequence=Not described;
 CC Name=E;
 CC IsoId=Q62959-4; Sequence=VSP_001709, VSP_001710;
 CC Name=F;
 CC IsoId=Q62959-5; Sequence=VSP_001711, VSP_001712;
 CC -!- TISSUE SPECIFICITY: Isoform B is expressed in kidney, liver, lung,
 CC ovary, spleen and uterus. Increased level in uterus during
 CC gestation. Isoform F is expressed at high levels in liver and
 CC spleen and less in brain, stomach, kidney, thymus, heart, lung and
 CC hypothalamus.
 CC -!- PTM: Phosphorylated on two tyrosine residues. Tyr-985 may be the
 CC major site of phosphorylation. Phosphorylation on both sites is
 CC required for full activity (By similarity).
 CC -!- DISEASE: The fatty (FA) mutation produces profound obesity of
 CC early onset caused by hyperphagia, defective nonshivering
 CC thermogenesis, and preferential deposition of energy into adipose
 CC tissue.
 CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
 CC Subfamily 2.
 CC -!- SIMILARITY: Contains 3 fibronectin type III domains.
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DR EMBL: AF287258; AAF89300.1; -.
DR EMBL: U53144; AAB03088.1; -.
DR EMBL: D84126; BAA12231.1; -.
DR EMBL: ABO11006; BAA24899.1; -.
DR EMBL: AF007818; AAB63201.1; -.
DR EMBL: AF007819; AAB63202.1; -.
DR EMBL: U67207; AAB40654.1; -.
DR EMBL: AF304191; AAG22823.1; -.
DR InterPro: IPR002996; CRA.
DR InterPro: IPR009957; FN III-like.
DR InterPro: IPR003961; FN III.
DR InterPro: IPR003529; Hemtopopn_L_F2.
DR Pfam: PF00041; fn3; 2.
DR PROSITE: PS01353; HEMATOPO REC L_F2; 1.
KW Obesity; Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
KW Alternative splicing; Phosphorylation; Polymorphism.
FT CHAIN 1 21
FT SIGNAL 22 1162
FT DOMAIN 22 839
FT TRANSMEM 840 860
FT DOMAIN 861 1162
FT DOMAIN 236 318
FT DOMAIN 535 621
FT DOMAIN 736 821
FT DOMAIN 737 90
FT DISULFID 89 99
FT DISULFID 131 142
FT DISULFID 186 195
FT DISULFID 188 193
FT DISULFID 350 410
FT DISULFID 411 416
FT DISULFID 471 526
FT DISULFID 486 496
FT CARBOHYD 55 55
FT CARBOHYD 56 56
FT CARBOHYD 73 73
FT CARBOHYD 98 98
FT CARBOHYD 187 187
FT CARBOHYD 275 275
FT CARBOHYD 345 345
FT CARBOHYD 356 356
FT CARBOHYD 431 431

Query Match 11.5%; Score 138; DB 1; Length 1162;
Best Local Similarity 30.9%; Pred. No. 0.00036;
Matches 56; Conservative 23; Mismatches 62; Indels 40; Gaps 11;

2y 39 LKO--EATSCSLHRSANATHATVTCMDVFH-----FMADDIFSVNITDQSGNYSOE 89
2b 177 LKDSFQTVQC-----NCVRECECHVPVPRAKVNVALLMYLEITSAGVSFQSLMSLQ 229
2y 90 CGSFLLAESIKAPP--FNVTVTFSGQYNISWRSDYEDPAPYMLKGKLYELQYRNGDP 147
2b 230 --PMLV---VKPDPPGLGRMEVTDGGLKISWDSQTKAPF-----PLQYQVYLENST- 277
2y 148 WAYSPPRKLKSVDSRSV-SLLPLEFRKDSSEYELQVRAGMPGSSYOGTWSWSDPVIFOT 206
2b 278 -IVREAAEIVSDTSLLDVSLP-----GSSIEYQVRSKRDLGS---GVWSDSLPOLFTT 328
2y 207 Q 207
2b 329 Q 329

RESULT 9
LEPR HUMAN STANDARD; PRT; 1165 AA.
AC P48357; Q13593; Q13594; Q92919; Q92920; Q92921;
JT 01-FEB-1996 (Rel. 33, Created)
JT 01-FEB-1996 (Rel. 33, Last sequence update)
JT 15-MAR-2004 (Rel. 43, Last annotation update)
2S Leptin receptor precursor (LEP-R) (OB-R) (Hub219).
3N LEP-R OR OBR OR DB.

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1] SEQUENCE FROM N.A. (ISOFORMS B AND E).
RC TISSUE=Brain;
RX MEDLINE=96128129; PubMed=8548812;
RA Tartaglia L.A., Dembeki M., Wang X., Deng N., Culpepper J.,
RA Devos R., Richards G.J., Campfield L.A., Clark F.T., Deeds J.,
RA Muir C., Sanker S., Moriarty A., Moore K.J., Smutko J.S.,
RA Mays G.G., Wolf E.A., Monroe C.A., Tepper R.I.;
RT "Identification and expression cloning of a leptin receptor, OB-R.";
RL Cell 83:1263-1271(1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS A; B AND C).
RC TISSUE=Fetal liver;
RX MEDLINE=96398968; PubMed=8805376;
RA Bennett B.D., Solar G.P., Yuan J.Q., Mathias J., Thomas G.R.,
RA Matthews W.;
RT "A role for leptin and its cognate receptor in hematopoiesis.";
RL Curr. Biol. 6:1170-1180(1996).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM B), AND VARIANTS ARG-109 AND ARG-223.
RX MEDLINE=97301763; PubMed=9158141;
RA Thompson D.B., Ravussin E., Bennett P.H., Bogardus C.;
RT "Structure and sequence variation at the human leptin receptor gene in
RT lean and obese Pima Indians.";
RL Hum. Mol. Genet. 6:675-679(1997).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM A).
RX MEDLINE=97215244; PubMed=9061609;
RA Luoh S.-M., Di Marco F., Levin N., Armanini M., Xie M.H., Nelson C.,
RA Bennett G.L., Williams M., Spencer S.A., Gurney A., de Sauvage F.J.;
RT "Cloning and characterization of a human leptin receptor using a
RT biologically active leptin immunoadhesin.";
RL J. Mol. Endocrinol. 18:77-85(1997).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORMS A; C AND D).
RX MEDLINE=96206286; PubMed=8616721;
RA Cioffi J.A., Shafer A.W., Zupancic T.J., Smith-Gbur J., Mikhail A.,
RA Platika D., Shodgrass H.R.;
RT "Novel B219/OB receptor isoforms: possible role of leptin in
RT hematopoiesis and reproduction.";
RL Nat. Med. 2:585-589(1996).
RN [6]
RP ALTERNATIVE SPLICING DUE TO AN ENDOGENOUS RETROVIRUS.
RX MEDLINE=99128223; PubMed=9929394;
RA Kapitonov V.V., Jurka J.;
RT "The long terminal repeat of an endogenous retrovirus induces
RT alternative splicing and encodes an additional carboxy-terminal
RT sequence in the human leptin receptor.";
RL J. Mol. Evol. 48:248-251(1999).
RN [7]
RP CARBOHYDRATE-LINKAGE SITES, DISULFIDE BONDS, AND PARTIAL SEQUENCE.
RX MEDLINE=99003211; PubMed=9786864;
RA Hanlu M., Arakawa T., Bures E.J., Young Y., Hui J.O., Rohde M.F.,
RA Welcher A.A., Horan T.;
RT "Human leptin receptor. Determination of disulfide structure and
RT N-glycosylation sites of the extracellular domain.";
RL J. Biol. Chem. 273:28691-28695(1998).
RN [8]
RP VARIANT ARG-223.
RX MEDLINE=96270489; PubMed=8666155;
RA Considine R.V., Considine E.L., Williams C.J., Hyde T.M., Caro J.F.;
RT "The hypothalamic leptin receptor in humans: identification of
RT incidental sequence polymorphisms and absence of the db/db mouse and
RL fa/fa rat mutations.";
RN Diabetes 45:992-994(1996).
RN [9]
RP VARIANTS ARG-109; ARG-204; ARG-223 AND ASN-656.
RX MEDLINE=97289527; PubMed=9144432;

```

RA Schwald S.M., Soerensen T.D., Soerensen T.I., Tybjaerg-Hansen A.,
 RA Andersen T., Chung W.K., Leibell R.L., Pedersen O.;
 RT "Amino acid variants in the human leptin receptor: lack of association
 to juvenile onset obesity.";
 RL Biochem. Biophys. Res. Commun. 233:248-252(1997).
 RN [10]
 RP VARIANTS ARG-109; ARG-223 AND ASN-656.
 RX MEDLINE=97431549; PubMed=9287054;
 RA Chung W.K., Power-Kehoe L., Chua M., Chu F., Aronne L., Huma Z.,
 RA Sothern M., Udall J.N., Kahle B., Leibell R.L.;
 RT "Exonic and intronic sequence variation in the human leptin receptor
 gene (LEPR).";
 RL Diabetes 46:1509-1511(1997).
 RN [11]
 RP VARIANTS ARG-109; ARG-223; ASN-656 AND THR-675.
 RX MEDLINE=97075638; PubMed=9860295;
 RA Roth H., Korn T., Rosenkranz K., Hinney A., Ziegler A., Kunz J.,
 RA Siegfried W., Mayer H., Hebebrand J., Grzeschik K.-H.;
 RT "Transmission disequilibrium and sequence variants at the leptin
 receptor gene in extremely obese German children and adolescents.";
 RL Hum. Genet. 103:540-546(1998).
 RN [12]
 RP VARIANTS ARG-109; ARG-223 AND ASN-656.
 RX MEDLINE=97318795; PubMed=9175732;
 RA Gotoda T., Manning B.S., Goldstone A.P., Imrie H., Evans A.L.,
 RA Strosberg A.D., McKeigue P.M., Scott J., Altman T.J.;
 RT "Leptin receptor gene variation and obesity: lack of association in a
 white British male population.";
 RL Hum. Mol. Genet. 6:869-876(1997).
 CC -!- FUNCTION: Receptor for obesity factor (leptin). Involved in the
 regulation of fat metabolism and in a hematopoietic pathway
 required for normal lymphopoiesis. May play a role in
 reproduction.
 CC -!- FUNCTION: The short form (isoform A) may act to transport leptin
 to the cerebrospinal fluid (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Except for form B
 which could be soluble.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=5;
 CC Name=B; Synonyms=13.2, OBRb;
 CC IsoId=P48357-1; SequencesDisplayed;
 CC Name=A; Synonyms=6.4, HuB219.3;
 CC IsoId=P48357-2; Sequences=VSP_001689, VSP_001690;
 CC Name=C; Synonyms=12.1, OBRa;
 CC IsoId=P48357-3; Sequences=VSP_001691, VSP_001692;
 CC Name=D; Synonyms=HuB219.2;
 CC IsoId=P48357-4; Sequences=VSP_001693, VSP_001694;
 CC Name=E;
 CC IsoId=P48357-5; Sequences=VSP_001688;
 CC -!- TISSUE SPECIFICITY: Isoform A expressed in fetal liver and in
 hematopoietic tissues and choroid plexus. In adults highest
 expression in heart, liver, small intestine, prostate and ovary.
 CC Low level in lung and kidney. Isoform B is highly expressed in
 hypothalamus.
 CC -!- DOMAIN: The cytoplasmic domain may be essential for intracellular
 signal transduction by activation of JAK tyrosine kinase and
 STATs.
 CC -!- PTM: Phosphorylated on two tyrosine residues. Tyr-986 may be the
 major site of phosphorylation. Phosphorylation on both sites is
 required for full activity (By similarity).
 CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
 CC Subfamily 2.
 CC -!- SIMILARITY: Contains 3 fibronectin type III domains.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 European Bioinformatics Institute. There are no restrictions on its
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 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
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DE antigen).
 DN IL4R OR IL4RA OR 582J2.1.
 DS Homo sapiens (Human).
 DC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 DC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 DX NCBI_TaxID=9606;
 DX [1]
 XP SEQUENCE FROM N.A.
 XC TISSUE=Peripheral blood;
 RA MEDLINE=90171849; PubMed=2307934;
 RA Idzerda R.L., March C.J., Mosley B., Lyman S.D., Bos T.V.,
 RA Gimpel S.D., Din W.S., Grabstein K.H., Widmer M.B., Park L.S.,
 RA Cosman D., Beckmann M.P.;
 RA "Human interleukin 4 receptor confers biological responsiveness and
 RT defines a novel receptor superfamily.";
 RL J. Exp. Med. 171:861-873 (1990).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=91120547; PubMed=2278997;
 RP Galizzi J.-P., Zuber C.E., Harada N., Gorman D.M., Djossou O.,
 RA Kastelein R., Banchereau J., Howard M., Miyajima A.;
 RA "Molecular cloning of a cDNA encoding the human interleukin 4
 RT receptor.";
 RL Int. Immunol. 2:669-675 (1990).
 RN [3]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=99425270; PubMed=10493829;
 RP Loftus B.J., Kim U.-J., Sredon V.P., Kalush F., Brandon R.,
 RA Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L.,
 RA Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S.,
 RA Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;
 RA "Genome duplications and other features in 12 Mb of DNA sequence from
 RT human chromosome 16p and 16q.";
 RL Genomics 60:295-308 (1999).
 RN [4]
 RN SEQUENCE FROM N.A.
 RP Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
 RA Nickerson D.A.;
 RA Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RN VARIANTS VAL-75; ALA-400; ARG-431; LEU-436 AND PRO-786.
 RP MEDLINE=97224413; PubMed=9070874;
 RP Deichmann K., Bardutzky J., Forster J., Heinzmann A., Kuehr J.;
 RA "Common polymorphisms in the coding part of the IL4-receptor gene.";
 RL Biochem. Biophys. Res. Commun. 231:696-697 (1997).
 RN [6]
 RN VARIANT ATOPIC ARG-576.
 RP MEDLINE=98041803; PubMed=9392697;
 RP Hershey G.K.K., Friedrich M.F., Esswein L.A., Thomas M.L.,
 RA Chatila T.A.;
 RA "The association of atopy with a gain-of-function mutation in the
 RT alpha subunit of the interleukin-4 receptor.";
 RL New Engl. J. Med. 337:1720-1725 (1997).
 RN [7]
 RN VARIANT ATOPIC ASTHMA VAL-75.
 RP MEDLINE=98282087; PubMed=9620765;
 RP Mitsuyasu H., Izuura K., Mao X.-Q., Gao P.S., Arinobu Y., Enomoto T.,
 RA Kawai M., Sasaki S., Dake Y., Hamasaki N., Shirakawa T., Hopkin J.M.;
 RA "Ile50Val variant of IL4R alpha upregulates IgE synthesis and
 RT associates with atopic asthma.";
 RL Nat. Genet. 19:119-120 (1998).
 RN [8]
 RN VARIANT ATOPIC ASTHMA VAL-75.
 RP MEDLINE=99322293; PubMed=10390422;
 RP Noguchi E., Shibasaki M., Arinami T., Takeda K., Yokouchi Y.,
 RA Kobayashi K., Imoto N., Nakahara S., Matsui A., Hamaguchi H.;
 RA "No association between atopy/asthma and the Ile50Val polymorphism of
 RT IL-4 receptor.";
 RL Am. J. Respir. Crit. Care Med. 160:342-345 (1999).
 RN [9]
 RN VARIANTS PRO-503 AND ARG-576.
 RP MEDLINE=99250314; PubMed=10233717;
 RP Kruse S., Japha T., Tedner M., Sparholt S.H., Forster J., Kuehr J.,
 RA

RA Deichmann K.A.;
 RT "The polymorphisms S503P and Q576R in the interleukin-4 receptor alpha
 RT gene are associated with atopy and influence the signal
 RT transduction.";
 RL Immunology 96:365-371 (1999).
 RN [10]
 RN VARIANT ALA-752.
 RX MEDLINE=20143377; PubMed=10677312;
 RX Ober C., Leavitt S.A., Tsalenko A., Howard T.D., Hoki D.M., Daniel R.,
 RA Newman D.L., Wu X., Parry R., Lester L.A., Solway J., Blumenthal M.,
 RA King R.A., Xu J., Meyers D.A., Bleeker E.R., Cox N.J.;
 RA "Variation in the interleukin 4-receptor alpha gene confers
 RT susceptibility to asthma and atopy in ethnically diverse
 RT populations.";
 RL Am. J. Hum. Genet. 66:517-526 (2000).
 RN [11]
 RN VARIANT ATOPIC DERMATITIS ARG-576.
 RX MEDLINE=20269830; PubMed=10809862;
 RX Oiso N., Fukai K., Ishii M.;
 RT "Interleukin 4 receptor alpha chain polymorphism Gln551Arg is
 RT associated with adult atopic dermatitis in Japan.";
 RL Br. J. Dermatol. 142:1003-1006 (2000).
 RN [12]
 RN VARIANT PRO-786.
 RX MEDLINE=21405389; PubMed=11513543;
 RX Andrews R.P., Burrell L., Rosa-Rosa L., Cunningham C.M.,
 RA Brzezinski J.L., Bernstein J.A., Khurana Herehey G.K.;
 RT "Analysis of the Ser786Pro interleukin-4 receptor alpha allelic
 RT variant in allergic and nonallergic asthma and its functional
 RT consequences.";
 RL Clin. Immunol. 100:298-304 (2001).
 RN [13]
 RN VARIANT ILE-579.
 RX MEDLINE=21182061; PubMed=11285129;
 RX Lozano F., Places L., Vila J.M., Padilla O., Arman M., Gimferrer I.,
 RA Suarez E., Lopez de la Iglesia A., Miserachs N., Vives J.; (Val554Ile)
 RT "Identification of a novel single-nucleotide polymorphism
 RT and definition of eight common alleles for human IL4RA exon 11.";
 RL Tissue Antigens 57:216-220 (2001).
 CC -!- FUNCTION: This is a receptor for interleukin 4. A soluble form
 CC of the IL4 receptor may represent a regulatory molecule specific
 CC for IL4-dependent immune responses.
 CC -!- SUBUNIT: Heterodimer of an alpha chain and a common gamma chain.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- DISEASE: Defects in IL4R are a cause of susceptibility to atopic
 CC asthma [MIM:147781].
 CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
 CC Subfamily 4.
 CC -!- DATABASE: NAME=PRO; NOTE=CD guide CD124 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd124.htm".
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X52425; CAA36672.1; -.
 CC EMBL; AC004525; AAC23495.1; -.
 CC EMBL; AF421855; AAL12163.1; -.
 CC PIR; A60386; A60386.
 CC PDB; 1IAR; 03-MAR-00.
 CC PDB; 1IRS; 15-MAY-97.
 CC PDB; 1ITE; 26-JAN-95.
 CC Genew; HGNC:6015; IL4R.
 CC MIM; 147781; -.
 CC GO; GO:0005887; C:integral to plasma membrane; TAS.
 CC GO; GO:0004913; P:interleukin-4 receptor activity; TAS.
 CC GO; GO:0005057; P:receptor signaling protein activity; TAS.
 CC GO; GO:0006935; P:immune response; TAS.
 CC GO; GO:0007165; P:signal transduction; TAS.


```

DR InterPro: IPR002996; CRIA.
DR InterPro: IPR008957; FN_III-like.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003531; Hemtopoptn_S_F1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Disease mutation;
KW Polymorphism; 3D-structure.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 825 INTERLEUKIN-4 RECEPTOR ALPHA CHAIN.
FT DOMAIN 26 232 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 233 256 POTENTIAL.
FT DOMAIN 257 825 CYTOPLASMIC (POTENTIAL).
FT DISULFID 34 44 BY SIMILARITY.
FT DISULFID 74 86 BY SIMILARITY.
FT CARBOHYD 53 93 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 98 98 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 128 128 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 134 134 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 176 176 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 209 209 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARIANT 75 75 I -> V (in atopic asthma; dbSNP:1805010).
FT VARIANT 400 400 E -> A (in dbSNP:1805011).
FT VARIANT 431 431 C -> R (in dbSNP:1805012).
FT VARIANT 436 436 S -> L (in dbSNP:1805013).
FT VARIANT 503 503 S -> P (in dbSNP:1805015).
FT VARIANT 576 576 O -> R (in atopic dermatitis; dbSNP:1801275).
FT VARIANT 579 579 V -> I.
FT VARIANT 752 752 S -> A (in dbSNP:1805016).
FT VARIANT 786 786 S -> P (in 1.8% of the population; dbSNP:1805014).
FT VARIANT 825 825 S -> A (in dbSNP:1805011).
SQ SEQUENCE 825 AA; 89658 MW; 9F886DF5612297F8 CRC64;
Query Match 11.3%; Score 135.5; DB 1; Length 825;
Best Local Similarity 26.0%; Pred. No. 0.00038;
Matches 57; Conservative 25; Mismatches 76; Indels 61; Gaps 12;
QY 6 CYTDVLTQVIGLENNLHPST-----LTLTQOQYELKDEATSCSLHSAHATHATY 60
DB 34 CVSDYMSITC-----EWMKNGPTNCSTELRLYLQVLF--LLSEATC-----IPENNGGAGC 84
QY 61 TCHMDVPHFMADDFSVNITDQSGNSDEC-----GSFLAESIKPAPPENVTV-- 109
DB 85 VCHL-----LMDVVVSAD-----NYTDLWAGQQLLWKGSKPSEHVXKPRAPGNLIVHT 133
QY 110 TFGQYNIWSRSDYEDPAFMYLKGQLQVELQVRNGDPWAVSPRRKLISVDVSRVSL 169
DB 134 NVSDTLTLTWSNPF--PPDNYLNHLTVAVNIWSENDP-----ADFRIYNYTYL 180
QY 170 E-----FEKDSGYELOVRAGMPGSSVCGTWSWS 199
DB 181 EPSLIAASTLKSIGSYRVRVRAW---AQCVNTTWSWS 216
RESULT 11
LEPR MACMU
ID LEPR MACMU STANDARD; PRT; 1163 AA.
AC Q9MYL0; Q9MYK9; Q9MYL1; Q9MYL2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Leptin receptor precursor (LEP-R) (OB-R).
GN LEPR OR OBR.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OC NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS A AND B).
RX MEDLINE=98408931; PubMed=9738551;
RA Hotta K., Gustafson T.A., Ortmeier H.K., Bodkin N.L., Hansen B.C.;
RT "Monkey leptin receptor mRNA: sequence, tissue distribution, and mRNA
RT expression in the adipose tissue of normal, hyperinsulinemic, and type
RL 2 diabetic rhesus monkeys.";
RN Obes. Res. 6:353-360(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS A AND B).
RX MEDLINE=98408931; PubMed=9738551;
RA Hotta K., Gustafson T.A., Ortmeier H.K., Bodkin N.L., Hansen B.C.;
RT "Monkey leptin receptor mRNA: sequence, tissue distribution, and mRNA
RT expression in the adipose tissue of normal, hyperinsulinemic, and type
RL 2 diabetic rhesus monkeys.";
RN Obes. Res. 6:353-360(1998).
RN [3]
RP SEQUENCE FROM N.A.
RX Gustafson T.A., Ortmeier H.K., Bodkin N.L., Hansen B.C.;
RA Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: Receptor for obesity factor (leptin). Involved in the
CC regulation of fat metabolism and in a hematopoietic pathway
CC required for normal lymphopoiesis. May play a role in
CC reproduction.
CC -I- FUNCTION: The short form (isoform A) may act to transport leptin
CC to the cerebrospinal fluid (By similarity).
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=B;
CC IsoId=Q9MYL0-1; Sequences=Displayed;
CC Name=A;
CC IsoId=Q9MYL0-2; Sequences=VSP_001695; VSP_001696;
CC -I- TISSUE SPECIFICITY: Widely expressed. High expression of isoform B
CC in liver, adipose tissue, hypothalamus and choroid plexus.
CC -I- DOMAIN: The cytoplasmic domain may be essential for intracellular
CC signal transduction by activation of JAK tyrosine kinase and
CC STATs.
CC -I- PTM: Phosphorylated on two tyrosine residues. Tyr-984 may be the
CC major site of phosphorylation. Phosphorylation on both sites is
CC required for full activity (By similarity).
CC -I- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC Subfamily 2.
CC -I- SIMILARITY: Contains 3 fibronectin type III domains.
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CC -----
CC EMBL; AF225874; AAF35388.1; -
CC EMBL; AF225875; AAF35389.1; -
CC EMBL; AF225876; AAF35387.1; -
CC EMBL; AF225877; AAF35388.1; -
CC HSSP; P16471; 1BP3.
CC InterPro; IPR002956; CRIA.
CC InterPro; IPR008957; FN_III-like.
CC InterPro; IPR003961; FN_III.
CC InterPro; IPR003529; Hemtopoptn_L_F2.
CC InterPro; IPR003531; Hemtopoptn_S_F1.
CC Pfam; PF00041; fn3; 2.
CC SMART; SM00060; FN3; 4.
CC PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
CC PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
KW Obesity; Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
KW Alternative splicing; Phosphorylation.
FT SIGNAL 1 21 POTENTIAL.

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CC -1- SIMILARITY; Belongs to the type I cytokine family of receptors.
CC Subfamily 4.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M55050; AAA41429.1; -.
CC DR HSPSP; P14784; IILM.
CC DR InterPro; IPR002996; CR1A.
CC DR InterPro; IPR008957; FN III-like.
CC DR InterPro; IPR003961; FN III.
CC DR InterPro; IPR003531; Hemtopoptn_s_F1.
CC DR SMART; SM00060; FN3; 1.
CC DR PROSITE; PS01355; HEMATOPO REC_S_F1; 1.
CC KM Receptor; Transmembrane; Glycoprotein; Signal.
CC FT SIGNAL 1 26 POTENTIAL.
CC FT CHAIN 27 537 INTERLEUKIN-2 RECEPTOR BETA CHAIN.
CC FT DOMAIN 27 239 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 240 267 POTENTIAL.
CC FT DOMAIN 268 537 CYTOPLASMIC (POTENTIAL).
CC FT DISULFID 36 46 BY SIMILARITY.
CC FT DISULFID 74 86 BY SIMILARITY.
CC FT CARBOHYD 43 43 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 55 55 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 71 71 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 150 150 N-LINKED (GLCNAC. .) (POTENTIAL).
CC SQ SEQUENCE 537 AA; 60657 MW; 9C744A24F3361968 CRC64;
CC -----
CC Query Match 11.2%; Score 134; DB 1; Length 537;
CC Best Local Similarity 23.1%; Pred.No.0.0003;
CC Matches 58; Conservative 41; Mismatches 72; Indels 80; Gaps 13;
CC -----
QY 1 CPDLVCYDTYLTQVICILEMWNLPSTLTTLTWQDYEEIKDEA---TSCSLHRSAH----- 53
DB 31 CSHLKCFYNSRANVSC---MWS-----PERRALNVTSCIHAKSMDRHW 70
QY 54 NAT-----HATYTCMH-----DVFHFMADDIFSVNIT--DOSGNYSQBCGSFLLAES 98
DB 71 NKTCELTPTVQASWAGNAILGLPLDPSQSLTSVDLSLVVCEEKGWRVKYCTTFPPDN 130
QY 99 IKDPAPPNVTVTF--SGQYNIWNR-----SDYEDDPAFYMLKGLQYELQYRNRGDPWAVSP 152
DB 131 LRLIAPHSLQLVLIHETRCNISWEVSQVSHYNP-----YLEFF-----A 170
QY 153 RRKLISVDSRSVLLPLEPK-----DSSYELOVRAGMPGSSYOGTWSESDPV 202
DB 171 RRLLDRSWEDASVFLSKORQWIFLETTPDTSYELOVRVIAQRKT--RTWSPWSQPM 228
QY 203 IFOTQSEELKE 213
DB 229 AFRTRPADPKK 239
CC -----
RESULT 13
CYRG_MOUSE
ID CYRG_MOUSE STANDARD; PRT; 369 AA.
AC P34902;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cytokine receptor common gamma chain precursor (Gamma-C)
DE (interleukin-2 receptor gamma chain) (IL-2R gamma chain) (P64).
DE IL2RG.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Theria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RX [1]

```

RP SEQUENCE FROM N.A.
 RX MEDLINE=93777575; PubMed=8503926;
 RA Kumaki S., Kondo M., Takeshita T., Aseo H., Nakamura M., Sugamura K.;
 RT "Cloning of the mouse interleukin 2 receptor gamma chain:
 demonstration of functional differences between the mouse and human
 receptors.";
 RL Biochem. Biophys. Res. Commun. 193:356-363(1993).
 RN (2)

RP SEQUENCE FROM N.A.
 RC STRAIN=CBA/CA;
 RX MEDLINE=93391374; PubMed=8378320;
 RA Cao X., Kozak C.A., Liu Y.J., Noguchi M., O'Connell E., Leonard W.J.;
 RT "Characterization of cDNAs encoding the murine interleukin 2 receptor
 (IL-2R) gamma chain: chromosomal mapping and tissue specificity of
 IL-2R gamma chain expression.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:8464-8468(1993).
 RN (3)

RP SEQUENCE FROM N.A.
 RX MEDLINE=93366191; PubMed=8359699;
 RA Kobayashi N., Nakagawa S., Minami Y., Taniguchi T., Kono T.;
 RT "Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor
 gamma.";
 RL Gene 130:303-304(1993).
 RN (4)

RP SEQUENCE FROM N.A.
 RX MEDLINE=95104285; PubMed=7805729;
 RA Disanto J.P., Certain S., Wilson A., MacDonald H.R., Avner P.,
 RA Fischer A., de Saint Basile G.;
 RT "The murine interleukin-2 receptor gamma chain gene: organization,
 chromosomal localization and expression in the adult thymus.";
 RL Eur. J. Immunol. 24:3014-3018(1994).
 RN (5)

RP SEQUENCE FROM N.A.
 RC STRAIN=B6.S;
 RX MEDLINE=96341745; PubMed=8750189;
 RA Chiu R.K., Droll A., Cooper D.L., Dougherty S.T., Dirks J.F.,
 RA Dougherty G.J.;
 RT "Molecular mechanisms regulating the hyaluronan binding activity of
 the adhesion protein CD44.";
 RL J. Neurooncol. 26:231-239(1995).
 RN (6)

RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Salivary gland;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Murley D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Common subunit for the receptors for a variety of
 interleukins.
 CC -!- SUBUNIT: The gamma chain is common to the IL2, IL4, IL7, IL12 and
 probably also the IL13 receptors.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
 CC -!- Subfamily 5.
 CC -!- SIMILARITY: Contains 1 fibronectin type III domain.

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CC EMBL; D13821; BAA02974.1; -
 CC EMBL; U21795; AAA64279.1; -
 CC EMBL; D13565; BAA02760.1; -
 CC EMBL; L20048; AAA39286.1; -
 CC EMBL; S75852; AAA32904.1; -
 CC EMBL; S75844; AAA32904.1; JOINED.
 CC EMBL; S75847; AAA32904.1; JOINED.
 CC EMBL; S75848; AAA32904.1; JOINED.
 CC EMBL; S75849; AAA32904.1; JOINED.
 CC EMBL; S75850; AAA32904.1; JOINED.
 CC EMBL; S75851; AAA32904.1; JOINED.
 CC EMBL; X75337; CAA53085.1; -
 CC EMBL; BC014720; AAH14720.1; -
 CC PIR; I49280; I49280.
 CC HSSP; P31785; IILM.
 CC MGD; MGI:96551; IL2rg.
 CC InterPro; IPR002996; CRJA.
 CC InterPro; IPR008957; FN_III-like.
 CC InterPro; IPR003961; FN_III.
 CC InterPro; IPR003531; Hemopoptn_S_Fl.
 CC Pfam; PF00041; fn3; 1.
 CC SMART; SM00060; FN3; 1.
 CC PROSITE; PS01355; HEMATOPO REC S_Fl; 1.
 CC Receptor; Transmembrane; Glycoprotein; Signal.
 CC SIGNAL 1 22
 CC BY SIMILARITY.
 CC CHAIN 23 369
 CC DOMAIN 23 263
 CC TRANSMEM 264 284
 CC DOMAIN 285 369
 CC DOMAIN 151 250
 CC DISULFID 62 72
 CC POTENTIAL.
 CC FT CARBOHYD 71 71
 CC CARBOHYD 75 75
 CC CARBOHYD 84 84
 CC CARBOHYD 96 96
 CC CARBOHYD 159 159
 CC CARBOHYD 164 164
 CC SEQUENCE 369 AA; 42241 MW; CB2D5AB459077AC7 CRC64;
 Query Match 11.2%; Score 133.5; DB 1; Length 369;
 Best Local Similarity 25.2%; Pred. No. 0.00021;
 Matches 56; Conservative 33; Mismatches 94; Indels 39; Gaps 12;
 QY 2 PDLVCYTDVLTQVICILEMWN--LHPSTLTITWQDQYELKDEAT--SCSLHSAHNAH 57
 DB 58 PEVQCFFVNIEMNC---IWNSSSEQATNLTHYRY-KVSDNNTFQECSHYLSKEITS 113
 QY 58 ATTTCMDVHFHMADDFISVNTDQSGNSQRCGSPILLAESIKPAPFNVT--FSGQY 115
 DB 114 G---COIQKEDIQYTFVYQLDPOKQPRVQKLNQLNQLVPRAPENLTLSNLS 170
 QY 116 NISWRSDYEDPAFYMLKKG-LOYELOYR-NRGDPNAV-----SPRRKLISVDSRSVSLIP 168
 DB 171 ELAKSEH-----IKERCLQVLQYRSNRDSRWTELIVNHEPRFSLFSVDE----- 216
 QY 169 LEFRKQSSLOVQVRAQPMGSSYQGTWSEWSDPVIFQTOSEE 210
 DB 217 ---LKRYTRVRSYRNPICGSSQ--WSKWSQFVHWSHTVE 253

RESULT 14
 TPOR_MOUSE
 ID TPOR_MOUSE STANDARD; PRT; 625 AA.

Q08351;
 01-FEB-1995 (Rel. 31, Created)
 01-FEB-1995 (Rel. 31, Last sequence update)
 15-MAR-2004 (Rel. 43, Last annotation update)
 Thrombopoietin receptor precursor (TPO-R) (Myeloproliferative leukemia protein) (C-mpl).
 3N MPL OR TPOR.
 3S Mus musculus (Mouse).
 3C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 3C Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 3X NCBI_TaxID=10090;
 [1]
 SEQUENCE FROM N.A.
 RX MEDLINE=93327753; PubMed=8334987;
 RA Skoda R.C., Seldin D.C., Chiang M.K., Peichel C.L., Vogt T.F.,
 RA Leder F.;
 RA "Murine c-mpl, a member of the hematopoietic growth factor receptor
 RT superfamily that transduces a proliferative signal.";
 RL EMBO J. 12:2645-2653(1993).
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=ICFW; TISSUE=Fetal liver;
 RX MEDLINE=93390934; PubMed=8397366;
 RA Vigon I., Florindo C., Fitchelson S., Guenet J.-L., Mattei M.-G.,
 RA Souyri M., Cosman D., Gisselbrecht S.;
 RT "Characterization of the murine Mpl proto-oncogene, a member of the
 RT hematopoietic cytokine receptor family: molecular cloning,
 RT chromosomal location and evidence for a function in cell growth.";
 RL Oncogene 8:2607-2615(1993).
 3C
 3C -!- FUNCTION: Receptor for thrombopoietin. May represent a regulatory
 3C molecule specific for TPO-R-dependent immune responses.
 3C -!- SUBCELLULAR LOCATION: Type I membrane protein.
 3C -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
 3C Subfamily 1.
 3C
 3C -!- SIMILARITY: Contains 2 fibronectin type III domains.
 3C
 3C This SWISS-PROT entry is copyright. It is produced through a collaboration
 3C between the Swiss Institute of Bioinformatics and the EMBL outstation -
 3C the European Bioinformatics Institute. There are no restrictions on its
 3C use by non-profit institutions as long as its content is in no way
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 3C or send an email to license@isb-sib.ch).
 3C
 3C EMBL; Z22649; CA80365.1; -;
 3C EMBL; Z22657; CA80372.1; -;
 3C EMBL; X73677; CA52031.1; -;
 3C PIR; S35317; S35317.
 3C PIR; S37622; S37622.
 3C HSP; P19235; IERN.
 3C MGD; MGI:197076; Mpl.
 3C InterPro; IPR002996; CR1A.
 3C InterPro; IPR003961; FN III.
 3C InterPro; IPR003528; Hemtopoptn_L_F1.
 3C Pfam; PF00041; fn3; 1.
 3C SMART; SM00060; FN3; 2.
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 3C Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 3C SIGNAL
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 Best Local Similarity 25.0%; Pred. No. 0.0005;
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 QY 62 -----CHM-----DVHFMAADDIFSVNITDQSGNYSQEGGS- 92
 DB 320 DPTWEKCEEBEPGSGQALVSRCHFKSRNDSVIHIL-----VEVITTAQGAHVSYLSP 373
 QY 93 FLAASI-KPAPPFNVTVPFGQVNIWSRSDYEDPAPFMLKGLQYLOYNRG-DFWAV 150
 DB 374 FWIHOAVLLPTPSLHWRVSSGRLEWQHOSWAA-----QETCYQLRYTGEGRDMKV 428
 QY 151 -SPRKLISVDSRSVSLPLFRKDSYVELQVRAGMPGSGSYQGTWSEWSDPVIFQOSE 209
 DB 429 LEP-----SLGARGGT---LRLRPARYSLQLRA-RLNGPTYQGPWASWPPARVSTGSE 479
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 ID LEPR_PIG STANDARD; Q95257; Q9N1P9; Q9XSN9;
 AC 002671; Q95257; Q9M2S2; Q9N1P9; Q9XSN9;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Leptin receptor precursor (LEP-R) (OB receptor) (OB-R).
 GN LEP-R OR OBR.
 OS Sus scrofa (pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OC NCBI_TaxID=9823;
 RX MEDLINE=20388825; PubMed=10911396;
 RA Ruiz-Cortes Z.T., Men T., Palin M.-F., Downey B.R., Lacroix D.A.,
 RA Murphy B.D.;
 RT "Porcine leptin receptor: molecular structure and expression in the
 RT ovary.";
 RL Mol. Reprod. Dev. 56:465-474(2000).
 RN [2]
 RC STRAIN=Yorkshire X Meishan.
 RA Lacroix D.A., Gevry N.Y., Ruiz-Cortes Z.T., Murphy B.D.;
 RT "Porcine leptin receptor intron 3, partial.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 7-854 FROM N.A.
 RC TISSUE=Liver;
 RA Hu X., Dai R., Li N., Wu C.;
 RT "Expression, detection, and partial cloning of porcine leptin receptor
 RT (OBR) gene.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 13-159 AND 916-1088 FROM N.A.
 RC TISSUE=Hypothalamus;
 RA Mattern R.L., Carroll J.A.;
 RT "Partial cDNA sequence of the porcine leptin receptor.";
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 109-123 FROM N.A.
 RX MEDLINE=99016721; PubMed=9600339;
 RA Strail A., Kopecky M., Moser G., Schroff J. Jr., Cepica S.;
 RT "HpaI and RsaI PCR-RFLPs within an intron of the porcine leptin
 RT receptor gene (LEPR) and its linkage mapping.";
 RL Anim. Genet. 29:405-406(1998).
 RN [6]
 RP SEQUENCE OF 408-470 FROM N.A.
 RX MEDLINE=97222487; PubMed=9069130;
 RA Ernst C.W., Kapke P.A., Yerle M., Rothschild M.F.;
 RT "The leptin receptor gene (LEPR) maps to porcine chromosome 6.";
 RL Mamm. Genome 8:226-226(1997).
 CC -!- FUNCTION: Receptor for obesity factor (leptin). Involved in the
 CC regulation of fat metabolism and in a hematopoietic pathway

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 3, 2004, 12:38:15 ; Search time 28.4967 Seconds
(without alignments)
1615.322 Million cell updates/sec

Title: US-09-825-561A-6
Perfect score: 1195
Sequence: 1 CPDLVCYTDYLTQVICILEM.....SDPVFOTQSEELKEGWPH 218

Scoring table: BLOSUM62
Gap 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
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2: /cgn2_6/ptodata/1/pubaa/PCT_NEW_PUB.pep:*
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13: /cgn2_6/ptodata/1/pubaa/US10A_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/1/pubaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1195	100.0	218	9	US-09-825-561A-6
2	1195	100.0	289	9	US-09-941-973-2
3	1195	100.0	538	9	US-09-965-313-2
4	1195	100.0	538	9	US-09-923-246-115
5	1195	100.0	538	9	US-09-825-561A-2
6	1195	100.0	538	10	US-09-972-218A-2
7	1195	100.0	538	14	US-10-264-634-2
8	1195	100.0	538	14	US-10-295-723-115
9	1195	100.0	538	14	US-10-482-622-115
10	1195	100.0	538	14	US-10-243-072-2
11	1195	100.0	538	14	US-10-414-186-2
12	1195	100.0	538	15	US-10-456-780-6
13	1195	100.0	567	9	US-09-825-561A-16
14	1195	100.0	606	9	US-09-923-246-97
15	1195	100.0	606	9	US-09-825-561A-30

16	1195	100.0	606	14	US-10-235-723-97	Sequence 97, Appl
17	1195	100.0	606	14	US-10-243-072-51	Sequence 51, Appl
18	1195	100.0	606	14	US-10-414-186-51	Sequence 51, Appl
19	1188	99.4	538	9	US-09-758-664-2	Sequence 2, Appl
20	1180	98.7	245	14	US-10-264-634-31	Sequence 31, Appl
21	1180	98.7	260	14	US-10-264-634-23	Sequence 23, Appl
22	1180	98.7	467	14	US-10-264-634-25	Sequence 25, Appl
23	1180	98.7	467	14	US-10-264-634-29	Sequence 23, Appl
24	1180	98.7	470	14	US-10-264-634-33	Sequence 33, Appl
25	1180	98.7	492	14	US-10-264-634-27	Sequence 27, Appl
26	1112	93.1	261	9	US-09-825-561A-71	Sequence 71, Appl
27	1077	90.1	247	9	US-09-825-561A-69	Sequence 69, Appl
28	1077	90.1	568	9	US-09-758-664-4	Sequence 4, Appl
29	1077	90.1	568	9	US-09-825-561A-65	Sequence 65, Appl
30	844	70.6	486	9	US-09-825-561A-73	Sequence 73, Appl
31	844	70.6	529	9	US-09-825-561A-12	Sequence 12, Appl
32	844	70.6	529	10	US-09-972-218A-10	Sequence 10, Appl
33	844	70.6	529	14	US-10-264-634-10	Sequence 10, Appl
34	844	70.6	529	14	US-10-243-072-85	Sequence 85, Appl
35	844	70.6	529	14	US-10-414-186-85	Sequence 85, Appl
36	844	70.6	529	15	US-10-418-450-2	Sequence 2, Appl
37	838	70.1	529	9	US-09-965-313-4	Sequence 4, Appl
38	838	70.1	529	9	US-09-732-234-6	Sequence 6, Appl
39	838	70.1	529	9	US-09-784-859-6	Sequence 6, Appl
40	838	70.1	529	13	US-10-076-840-6	Sequence 6, Appl
41	838	70.1	529	15	US-10-624-044-6	Sequence 6, Appl
42	829	69.4	240	14	US-10-264-634-35	Sequence 35, Appl
43	829	69.4	255	14	US-10-264-634-37	Sequence 37, Appl
44	829	69.4	260	14	US-10-264-634-39	Sequence 39, Appl
45	400	33.5	397	14	US-10-243-072-81	Sequence 81, Appl

ALIGNMENTS

RESULT 1
US-09-825-561A-6
; Sequence 6, Application US/09825561A
; Patent No. US20020137677A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. US20020137677A1ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHAL1 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-561A-6

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Best Local Similarity	100.0%;	Pred. No. 7e-118;		
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			Indels	0;
			Gaps	0;
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QY 121 SYEDPAFYMLKGKLOYELQYRNRPWAVSPRRKLIISVDSRSVSLLPLEFRKDSYELQ 180
Db 121 SYEDPAFYMLKGKLOYELQYRNRPWAVSPRRKLIISVDSRSVSLLPLEFRKDSYELQ 180
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RESULT 2

US-09-941-973-2
; Sequence 2, Application US/09941973
; Patent No. US20020160451A1
; GENERAL INFORMATION:
; APPLICANT: Maslakowski et al.
; TITLE OF INVENTION: NOVEL ORPHAN RECEPTORS
; FILE REFERENCE: REG650
; CURRENT APPLICATION NUMBER: US/09/941,973
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US/09/128,820
; PRIOR FILING DATE: 1998-08-04
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-941-973-2

Query Match 100.0%; Score 1195; DB 9; Length 289;
Best Local Similarity 100.0%; Pred. No. 1e-117;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 80 TCHMDVFHFMAADDIFSVNITDQSGNYSQCGSFLLAESIKPAPPFNVTTFSGQYNISWR 139
QY 121 SYEDPAFYMLKGKLOYELQYRNRPWAVSPRRKLIISVDSRSVSLLPLEFRKDSYELQ 180
Db 140 SYEDPAFYMLKGKLOYELQYRNRPWAVSPRRKLIISVDSRSVSLLPLEFRKDSYELQ 199
QY 181 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEBELKEGWNPH 218
Db 200 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEBELKEGWNPH 237

RESULT 3

US-09-965-313-2
; Sequence 2, Application US/09965313
; Patent No. US20020090680A1
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; TITLE OF INVENTION: NO. US20020090680A1 IL-9/IL-2 Receptor-Like Molecules
; FILE REFERENCE: and Uses Thereof
; FILE REFERENCE: 5800-17A
; CURRENT APPLICATION NUMBER: US/09/965,313
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 09/313,913
; PRIOR FILING DATE: 1999-05-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens IL-2/IL-9 Receptor Like
US-09-965-313-2

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Best Local Similarity 100.0%; Pred. No. 2.4e-117;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 4

US-09-923-246-115
; Sequence 115, Application US/09923246
; Patent No. US20020128446A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020128446Alak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-03-11
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-246-115

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Db 20 CPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDQYEELEKDEATSCSLHRSAHNATHATY 79
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Db 80 TCHMDVFHFMAADDIFSVNITDQSGNYSQCGSFLLAESIKPAPPFNVTTFSGQYNISWR 139
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Db 140 SYEDPAFYMLKGKLOYELQYRNRPWAVSPRRKLIISVDSRSVSLLPLEFRKDSYELQ 199
QY 181 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEBELKEGWNPH 218
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RESULT 5

US-09-825-561A-2
; Sequence 2, Application US/09825561A
; Patent No. US20020137677A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. US20020137677A1ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHAL CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825.561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-561A-2

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Best Local Similarity 100.0%; Pred. No. 2.4e-117;
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DB 80 TCHMDVHFHMADDDIFSVNITDQSGNYSQECGFLLAESIKPAPPFNVTTFSGQYNISWR 139
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QY 181 VRAGMPGSSYQGTWSEWSDPVIFQTQSEELKEGNPH 218
DB 200 VRAGMPGSSYQGTWSEWSDPVIFQTQSEELKEGNPH 237

RESULT 6

US-09-972-218A-2
; Sequence 2, Application US/09972218A
; Publication No. US20030049798A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Laura
; APPLICANT: Whitters, Matthew J
; APPLICANT: Collins, Mary
; APPLICANT: Young, Deborah A.
; APPLICANT: Donaldson, Debra D.
; APPLICANT: Lowe, Leslie D.
; APPLICANT: Unger, Michelle
; TITLE OF INVENTION: MU-1, Member of the Cytokine Receptor Family
; FILE REFERENCE: 22058-552CIP2
; CURRENT APPLICATION NUMBER: US/09/972,218A
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: 09/569384
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: 09/560766
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US/6057128
; PRIOR FILING DATE: 1998-03-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Human
US-09-972-218A-2

Query Match 100.0%; Score 1195; DB 10; Length 538;
Best Local Similarity 100.0%; Pred. No. 2.4e-117;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDQYBELKDEATSCSLHRSAHNATHATY 60
DB 20 CPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDQYBELKDEATSCSLHRSAHNATHATY 79
QY 61 TCHMDVHFHMADDDIFSVNITDQSGNYSQECGFLLAESIKPAPPFNVTTFSGQYNISWR 120
DB 80 TCHMDVHFHMADDDIFSVNITDQSGNYSQECGFLLAESIKPAPPFNVTTFSGQYNISWR 139
QY 121 SYEDPAPFYMKGKLOYELQYRNRGDPWAVSPRKLISVDSRSVSLLEPRKDSSEYELQ 180
DB 140 SYEDPAPFYMKGKLOYELQYRNRGDPWAVSPRKLISVDSRSVSLLEPRKDSSEYELQ 199
QY 181 VRAGMPGSSYQGTWSEWSDPVIFQTQSEELKEGNPH 218
DB 200 VRAGMPGSSYQGTWSEWSDPVIFQTQSEELKEGNPH 237

RESULT 7

US-10-264-634-2
; Sequence 2, Application US/10264634
; Publication No. US20030108549A1
; GENERAL INFORMATION:
; APPLICANT: Donaldson, Debra et al.
; TITLE OF INVENTION: Methods and Compositions for Modulating Interleukin-21 Receptor A
; FILE REFERENCE: G15320-P3
; CURRENT APPLICATION NUMBER: US/10/264,634
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: 09/040,005
; PRIOR FILING DATE: 1998-03-17
; PRIOR APPLICATION NUMBER: 09/560,766
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/569,384
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: 09/972,218
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/373,746
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Human
US-10-264-634-2

Query Match 100.0%; Score 1195; DB 14; Length 538;
Best Local Similarity 100.0%; Pred. No. 2.4e-117;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDQYBELKDEATSCSLHRSAHNATHATY 60
DB 20 CPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDQYBELKDEATSCSLHRSAHNATHATY 79
QY 61 TCHMDVHFHMADDDIFSVNITDQSGNYSQECGFLLAESIKPAPPFNVTTFSGQYNISWR 120
DB 80 TCHMDVHFHMADDDIFSVNITDQSGNYSQECGFLLAESIKPAPPFNVTTFSGQYNISWR 139
QY 121 SYEDPAPFYMKGKLOYELQYRNRGDPWAVSPRKLISVDSRSVSLLEPRKDSSEYELQ 180
DB 140 SYEDPAPFYMKGKLOYELQYRNRGDPWAVSPRKLISVDSRSVSLLEPRKDSSEYELQ 199
QY 181 VRAGMPGSSYQGTWSEWSDPVIFQTQSEELKEGNPH 218

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Db 200 VRAGPMGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237

RESULT 8
US-10-295-723-115
; Sequence 115, Application US/10295723
; Publication No. US20030125524A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030125524Alak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-723-115

Query Match 100.0%; Score 1195; DB 14; Length 538;
Best Local Similarity 100.0%; Pred. No. 2.4e-117;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCYTYDYLQTVICILEMWNHLPSTLTITWQDYEEELKDEATSCSLHRSAAHATHATY 60
Db 20 CPDLVCYTYDYLQTVICILEMWNHLPSTLTITWQDYEEELKDEATSCSLHRSAAHATHATY 79
QY 61 TCHMDVFHFMAADDIFSVNITDQSGNYSCGSGFLAESIKPAPPNVTVTFSGQYNISWR 120
Db 80 TCHMDVFHFMAADDIFSVNITDQSGNYSCGSGFLAESIKPAPPNVTVTFSGQYNISWR 139
QY 121 SYEDPAFYMLKGKQLQYELQYRNRPDPWAVSPRRKLISVDSRSVSLLEPRKDSYELQ 180
Db 140 SYEDPAFYMLKGKQLQYELQYRNRPDPWAVSPRRKLISVDSRSVSLLEPRKDSYELQ 199
QY 181 VRAGPMGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
Db 200 VRAGPMGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237

RESULT 9
US-10-282-622-16
; Sequence 16, Application US/10282622
; Publication No. US20030134390A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: West, James W.
; APPLICANT: No. US20030134390Alak, Julia E.
; TITLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS
; FILE REFERENCE: 01-37
; CURRENT APPLICATION NUMBER: US/10/282,622
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 60/337,586
; PRIOR FILING DATE: 2001-11-05
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; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-622-16

Query Match 100.0%; Score 1195; DB 14; Length 538;
Best Local Similarity 100.0%; Pred. No. 2.4e-117;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCYTYDYLQTVICILEMWNHLPSTLTITWQDYEEELKDEATSCSLHRSAAHATHATY 60
Db 20 CPDLVCYTYDYLQTVICILEMWNHLPSTLTITWQDYEEELKDEATSCSLHRSAAHATHATY 79
QY 61 TCHMDVFHFMAADDIFSVNITDQSGNYSCGSGFLAESIKPAPPNVTVTFSGQYNISWR 120
Db 80 TCHMDVFHFMAADDIFSVNITDQSGNYSCGSGFLAESIKPAPPNVTVTFSGQYNISWR 139
QY 121 SYEDPAFYMLKGKQLQYELQYRNRPDPWAVSPRRKLISVDSRSVSLLEPRKDSYELQ 180
Db 140 SYEDPAFYMLKGKQLQYELQYRNRPDPWAVSPRRKLISVDSRSVSLLEPRKDSYELQ 199
QY 181 VRAGPMGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
Db 200 VRAGPMGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237

RESULT 10
US-10-243-072-2
; Sequence 2, Application US/10243072
; Publication No. US20030148447A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: No. US20030148447Alak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZALPHA11
; FILE REFERENCE: 98-55C1
; CURRENT APPLICATION NUMBER: US/10/243,072
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/628,127
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: 1999-07-06
; PRIOR APPLICATION NUMBER: US 09/404,641
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-243-072-2

Query Match 100.0%; Score 1195; DB 14; Length 538;
Best Local Similarity 100.0%; Pred. No. 2.4e-117;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCYTYDYLQTVICILEMWNHLPSTLTITWQDYEEELKDEATSCSLHRSAAHATHATY 60
Db 20 CPDLVCYTYDYLQTVICILEMWNHLPSTLTITWQDYEEELKDEATSCSLHRSAAHATHATY 79
QY 61 TCHMDVFHFMAADDIFSVNITDQSGNYSCGSGFLAESIKPAPPNVTVTFSGQYNISWR 120
Db 80 TCHMDVFHFMAADDIFSVNITDQSGNYSCGSGFLAESIKPAPPNVTVTFSGQYNISWR 139
QY 121 SYEDPAFYMLKGKQLQYELQYRNRPDPWAVSPRRKLISVDSRSVSLLEPRKDSYELQ 180
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Db 140 SYEDPAPYMLKGKQLQYELQYRNRGDPWAVSPRKLISVDSRSVSLPLLEFRKDSSEYELQ 199
2y 181 VRAGMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
Db 200 VRAGMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237

RESULT 11
US-10-414-186-2
; Sequence 2, Application US/10414186
; Publication No. US2003017582SA1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: No. US2003017582SA1ak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZALPHAL1
; FILE REFERENCE: 98-55
; CURRENT APPLICATION NUMBER: US/10/414,186
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US/09/404,641
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-414-186-2

Query Match 100.0%; Score 1195; DB 14; Length 538;
Best Local Similarity 100.0%; Pred. No. 2.4e-117;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2y 1 CPDLVCYTDYLTQVICILEMWNLHPSTLTITWQOYBELKDEATCSLHSAHNATHATY 60
2b 20 CPDLVCYTDYLTQVICILEMWNLHPSTLTITWQOYBELKDEATCSLHSAHNATHATY 79
2y 61 TCHMDVHFHMADDIFSNITDQSGNYSQECGFLAESIKPAPPFNVTVPFGQYNISWR 120
2b 80 TCHMDVHFHMADDIFSNITDQSGNYSQECGFLAESIKPAPPFNVTVPFGQYNISWR 139
2y 121 SYEDPAPYMLKGKQLQYELQYRNRGDPWAVSPRKLISVDSRSVSLPLLEFRKDSSEYELQ 180
2b 140 SYEDPAPYMLKGKQLQYELQYRNRGDPWAVSPRKLISVDSRSVSLPLLEFRKDSSEYELQ 199
2y 181 VRAGMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
2b 200 VRAGMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237

RESULT 12
US-10-456-780-6
; Sequence 6, Application US/10456780
; Publication No. US20040009150A1
; GENERAL INFORMATION:
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Hughes, Steven D.
; APPLICANT: Holly, Richard D.
; TITLE OF INVENTION: USE OF IL-21 IN CANCER AND
; FILE REFERENCE: 03-08
; CURRENT APPLICATION NUMBER: US/10/456,780
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/387,127
; PRIOR FILING DATE: 2002-06-07
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; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-456-780-6

Query Match 100.0%; Score 1195; DB 15; Length 538;
Best Local Similarity 100.0%; Pred. No. 2.4e-117;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CPDLVCYTDYLTQVICILEMWNLHPSTLTITWQOYBELKDEATCSLHSAHNATHATY 60
Db 20 CPDLVCYTDYLTQVICILEMWNLHPSTLTITWQOYBELKDEATCSLHSAHNATHATY 79
Qy 61 TCHMDVHFHMADDIFSNITDQSGNYSQECGFLAESIKPAPPFNVTVPFGQYNISWR 120
Db 80 TCHMDVHFHMADDIFSNITDQSGNYSQECGFLAESIKPAPPFNVTVPFGQYNISWR 139
Qy 121 SYEDPAPYMLKGKQLQYELQYRNRGDPWAVSPRKLISVDSRSVSLPLLEFRKDSSEYELQ 180
Db 140 SYEDPAPYMLKGKQLQYELQYRNRGDPWAVSPRKLISVDSRSVSLPLLEFRKDSSEYELQ 199
Qy 181 VRAGMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
Db 200 VRAGMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237

RESULT 13
US-09-825-561A-16
; Sequence 16, Application US/09825561A
; Patent No. US20020137677A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. US20020137677Alak, Julia B.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHAL1 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: soluble zalphal1r/IgGammal polypeptide
US-09-825-561A-16

Query Match 100.0%; Score 1195; DB 9; Length 567;
Best Local Similarity 100.0%; Pred. No. 2.6e-117;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CPDLVCYTDYLTQVICILEMWNLHPSTLTITWQOYBELKDEATCSLHSAHNATHATY 60
Db 20 CPDLVCYTDYLTQVICILEMWNLHPSTLTITWQOYBELKDEATCSLHSAHNATHATY 79
Qy 61 TCHMDVHFHMADDIFSNITDQSGNYSQECGFLAESIKPAPPFNVTVPFGQYNISWR 120
Db 80 TCHMDVHFHMADDIFSNITDQSGNYSQECGFLAESIKPAPPFNVTVPFGQYNISWR 139
Qy 121 SYEDPAPYMLKGKQLQYELQYRNRGDPWAVSPRKLISVDSRSVSLPLLEFRKDSSEYELQ 180
Db 140 SYEDPAPYMLKGKQLQYELQYRNRGDPWAVSPRKLISVDSRSVSLPLLEFRKDSSEYELQ 199
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QY 181 VRAGPMFGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
Db 200 VRAGPMFGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237

RESULT 14

US-09-923-246-97
; Sequence 97, Application US/09923246
; Patent No. US20020128446A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020128446Alak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 97
; LENGTH: 606
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MBP-zalphal1 soluble receptor polypeptide sequence

US-09-923-246-97
Query Match 100.0%; Score 1195; DB 9; Length 606;
Best Local Similarity 100.0%; Pred. No. 2.8e-117;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CPDLVCYTDYLTQVICILEMWNLHPSTLTLTWQDQVEELKDEATCSLHRSAHNATHATY 60
Db 389 CPDLVCYTDYLTQVICILEMWNLHPSTLTLTWQDQVEELKDEATCSLHRSAHNATHATY 448
QY 61 TCHMDVFHFMAADIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTTFSGQYNISWR 120
Db 449 TCHMDVFHFMAADIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTTFSGQYNISWR 508
QY 121 SDYEDPAFYMLKGKLOYELQYRNRGDPWAVSPRRKLISVDSRSVSLPLEFRKDSSEYELQ 180
Db 509 SDYEDPAFYMLKGKLOYELQYRNRGDPWAVSPRRKLISVDSRSVSLPLEFRKDSSEYELQ 568
QY 181 VRAGPMFGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
Db 569 VRAGPMFGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 606
Search completed: March 3, 2004, 12:50:51
Job time : 28.4967 secs

US-09-923-246-97
Query Match 100.0%; Score 1195; DB 9; Length 606;
Best Local Similarity 100.0%; Pred. No. 2.8e-117;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CPDLVCYTDYLTQVICILEMWNLHPSTLTLTWQDQVEELKDEATCSLHRSAHNATHATY 60
Db 389 CPDLVCYTDYLTQVICILEMWNLHPSTLTLTWQDQVEELKDEATCSLHRSAHNATHATY 448
QY 61 TCHMDVFHFMAADIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTTFSGQYNISWR 120
Db 449 TCHMDVFHFMAADIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTTFSGQYNISWR 508
QY 121 SDYEDPAFYMLKGKLOYELQYRNRGDPWAVSPRRKLISVDSRSVSLPLEFRKDSSEYELQ 180
Db 509 SDYEDPAFYMLKGKLOYELQYRNRGDPWAVSPRRKLISVDSRSVSLPLEFRKDSSEYELQ 568
QY 181 VRAGPMFGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
Db 569 VRAGPMFGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 606

RESULT 15

US-09-825-561A-30
; Sequence 30, Application US/09825561A
; Patent No. US20020137677A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. US20020137677Alak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.

; TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 606
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MBP-human zalphal1 soluble receptor fusion
; OTHER INFORMATION: polypeptide
; US-09-825-561A-30

Query Match 100.0%; Score 1195; DB 9; Length 606;
Best Local Similarity 100.0%; Pred. No. 2.8e-117;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CPDLVCYTDYLTQVICILEMWNLHPSTLTLTWQDQVEELKDEATCSLHRSAHNATHATY 60
Db 389 CPDLVCYTDYLTQVICILEMWNLHPSTLTLTWQDQVEELKDEATCSLHRSAHNATHATY 448
QY 61 TCHMDVFHFMAADIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTTFSGQYNISWR 120
Db 449 TCHMDVFHFMAADIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTTFSGQYNISWR 508
QY 121 SDYEDPAFYMLKGKLOYELQYRNRGDPWAVSPRRKLISVDSRSVSLPLEFRKDSSEYELQ 180
Db 509 SDYEDPAFYMLKGKLOYELQYRNRGDPWAVSPRRKLISVDSRSVSLPLEFRKDSSEYELQ 568
QY 181 VRAGPMFGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
Db 569 VRAGPMFGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 606

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OM protein - protein search, using sw model

Run on: March 3, 2004, 12:24:04 ; Search time 52.0065 Seconds
(without alignments)
1184.377 Million cell updates/sec

Title: US-09-825-561A-6

Perfect score: 1195

Sequence: 1 CPDLVCVTDYLTQVTCILEM.....SDPVFQTQSEELKGNPNH 218

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_29Jan04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1195	100.0	289	3	AAy45029 HUMAN Orp
3	1195	100.0	361	3	AAy69883 Human hae
4	1195	100.0	538	2	AAy27450 Human MU-
5	1195	100.0	538	2	AAb18634 A human z
6	1195	100.0	538	3	AAy45031 HUMAN Orp
7	1195	100.0	538	3	AAy69886 Human hae
8	1195	100.0	538	3	AAy79312 Human cyt
9	1195	100.0	538	4	AAb48001 Human IL-
10	1195	100.0	538	5	AAb81960 Human 164
11	1195	100.0	538	5	AAu11912 Human MU-
12	1195	100.0	538	5	AAe13726 Human sol
13	1195	100.0	538	5	AAu11978 Human zal
14	1195	100.0	538	6	ABR61402 Human IL-
15	1195	100.0	538	6	AAe14939 Human int
16	1195	100.0	538	7	ABu62888 Human MU-
17	1195	100.0	538	7	ABw00881 Human cyt
18	1195	100.0	567	5	AAe13733 Human aci
19	1195	100.0	606	3	AAb18629 Amino aci
20	1195	100.0	606	3	AAy79316 Maltose b
21	1195	100.0	606	5	AAe13736 Maltose b
22	1195	100.0	606	5	AAu11973 MBP-human
23	1195	100.0	606	7	ABw00884 Human zal
24	1188	99.4	538	3	AAy94304 Human HNO
25	1188	99.4	538	4	AAu08728 Human HNO

26	1187	99.3	471	3	AAy45030	OCR
27	1180	98.7	245	6	ABR61414	Human IL-
28	1180	98.7	260	6	ABR61410	Human IL-
29	1180	98.7	467	6	ABR61413	Human IL-
30	1180	98.7	467	6	ABR61411	Human IL-
31	1180	98.7	470	6	ABR61415	Human IL-
32	1180	98.7	492	6	ABR61412	Human IL-
33	1170	97.9	538	4	AAE02459	Human DNA
34	1159	97.0	538	3	AAy69888	Mouse hae
35	1145	95.8	460	3	AAy69890	Human NR8
36	1138	95.2	375	3	AAy69889	Human NR8
37	1132	93.1	261	5	AAE13742	Human var
38	1077	90.1	247	5	AAE13740	Human HNO
39	1077	90.1	568	3	AAy94305	Human HNO
40	1077	90.1	568	4	AAE02457	Human DNA
41	1077	90.1	568	4	AAU08729	Human HNO
42	1077	90.1	568	5	AAe13738	Human sol
43	844	70.6	486	5	AAE13743	Mouse zal
44	844	70.6	529	3	AAy79320	Mouse cyt
45	844	70.6	529	5	AAu11915	Mouse MO-

ALIGNMENTS

RESULT 1

AAE13728

ID AAE13728 standard; protein; 218 AA.

XX AC AAE13728;

XX AC AAE13728;

DT 26-FEB-2002 (first entry)

XX DT 26-FEB-2002 (first entry)

XX DE Human soluble Zalphall cytokine receptor protein fragment.

XX Human; Zalphall; cytokine receptor; immunosuppressive; cytostatic;
KW inflammatory disorder; haemostatic; cell proliferation; immune disorder;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
KW myasthenia gravis; systemic lupus erythematosus; SLE; diabetes; aschma;
KW ulcerative colitis; inflammatory bowel disease; Crohn's disease; sepsis;
KW viral infection.

XX OS Homo sapiens.

XX PN WO200177171-A2.

XX PD 18-OCT-2001.

XX PF 03-APR-2001; 2001WO-US010872.

XX PR 05-APR-2000; 2000US-0194731P.

XX PR 28-JUL-2000; 2000US-0222121P.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Sprecher CA, Novak JE, West JW, Presnell SR, Holly RD, Nelson AJ;

XX DR WPI; 2002-025898/03.

XX DR N-PSDB; AAD22920.

XX Novel soluble receptor polypeptides and polynucleotides used as cytokine
PT antagonist for stimulating ligand activity-induced proliferation of
PT haematopoietic cells and for suppressing immune response in a mammal.
XX Claim 27; Page 176-178; 243pp; English.

XX The invention relates to an isolated soluble zalphall cytokine receptor
XX polypeptide and their cDNA molecules. Zalpha proteins are useful for
XX inhibiting or antagonising the ligand activity-induced proliferation of
XX haematopoietic cells and haematopoietic cell progenitors preferably
XX lymphoid cells which are natural killer cells or cytotoxic T cells.
XX Zalphall is useful for treating immune and inflammatory disorders, for
XX reducing proliferation of neoplastic B or T cells, for suppressing an

CC immune response in a mammal exposed to an antigen or pathogen. Zalpha is
 CC useful for treating diseases that require immune regulation including
 CC autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,
 CC myasthenia gravis, systemic lupus erythematosus (SLE) and diabetes;
 CC asthma, ulcerative colitis, inflammatory bowel disease, Crohn's disease,
 CC sepsis, viral infection (dengue virus infection) and cancer. The present
 CC sequence is human soluble Zalpha cytokine receptor protein fragment
 XX
 SQ Sequence 218 AA;

Query Match 100.0%; Score 1195; DB 5; Length 218;
 Best Local Similarity 100.0%; Pred. No. 4.3e-115;
 Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCYTDYLTQVICILEMNLHPSTLTITWQDQYEELKDEATCSLHRSAHNATHATY 60
 DB 1 CPDLVCYTDYLTQVICILEMNLHPSTLTITWQDQYEELKDEATCSLHRSAHNATHATY 60
 QY 61 TCHMDVHFHFWADDFISVNTDQSGNYSQCGSFLLAESIKPAPPFNVTTFSGQYNISWR 120
 DB 61 TCHMDVHFHFWADDFISVNTDQSGNYSQCGSFLLAESIKPAPPFNVTTFSGQYNISWR 120
 QY 121 SDYEDPAFYMLKGLQYELQYRNRPWAVSPRKLISVDSRSVSLLPLEFRKDSSEYELQ 180
 DB 121 SDYEDPAFYMLKGLQYELQYRNRPWAVSPRKLISVDSRSVSLLPLEFRKDSSEYELQ 180
 QY 181 VRAGPMGSSYQGTWSEWSDPVIFQTSBELKEGWNPH 218
 DB 181 VRAGPMGSSYQGTWSEWSDPVIFQTSBELKEGWNPH 218

RESULT 2
 AAY45029
 ID AAY45029 standard; protein; 289 AA.

XX AAY45029;

XX 31-MAY-2000 (first entry)

XX HUMAN Orphan Cytokine Receptor-10 (OCR10) polypeptide.

XX Human; Orphan Cytokine Receptor-10; OCR10; chromosome 16p12; cytokine;
 XX screen; cognate ligand; treatment; endocrine disorder; immune disorder.

XX Homo sapiens.

XX Key Location/Qualifiers
 XX Peptide 4..21
 XX /label= Signal_peptide
 XX Protein 22..289
 XX /label= Mature_HUMAN_OCR10
 XX Region 118..169
 XX /label= Proline_hinge_motif_region
 XX Domain 122..123
 XX /label= Proline_hinge_motif
 XX Domain 238..255
 XX /label= Transmembrane_domain
 XX /note= "Putative and hydrophobic"
 XX Region 263..278
 XX /label= Jak-binding_region
 XX /note= "Potential"

XX WO200008152-A1.

XX 17-FEB-2000.

XX 16-JUL-1999; 99WO-US016060.

XX 04-AUG-1998; 98US-00128820.

XX (REGE-) REGENERON PHARM INC.

XX Masiakowski PJ, Morris J, Valenzuela DM;

XX WPI; 2000-205707/18.
 DR N-PSDB; AAZ50746.
 XX New HUMAN orphan cytokine receptors 10 and 10-A useful for screening for
 PT drugs e.g. receptor agonists that may mediate survival and
 PT differentiation in cells naturally expressing the receptor and for
 PT screening for cognate ligands.

XX Example 1; Page 21; 54pp; English.

XX The present sequence is the HUMAN Orphan Cytokine Receptor-10 (OCR10)
 CC polypeptide. HUMAN OCR10 gene is located on chromosome 16p12. It is
 CC expressed at high levels in spleen, thymus, peripheral blood leucocytes
 CC and lymph nodes and moderately in heart and placenta. It has a role in
 CC immune system and cytokine function. It is useful in screening for
 CC cognate ligands or drugs that mediate survival and differentiation of
 CC cells expressing this receptor. Modified HUMAN OCR10 or its agonist can
 CC be used in the treatment of endocrine or immune disorders

XX Sequence 289 AA;

Query Match 100.0%; Score 1195; DB 3; Length 289;

Best Local Similarity 100.0%; Pred. No. 6.4e-115;

Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCYTDYLTQVICILEMNLHPSTLTITWQDQYEELKDEATCSLHRSAHNATHATY 60
 DB 20 CPDLVCYTDYLTQVICILEMNLHPSTLTITWQDQYEELKDEATCSLHRSAHNATHATY 79
 QY 61 TCHMDVHFHFWADDFISVNTDQSGNYSQCGSFLLAESIKPAPPFNVTTFSGQYNISWR 120
 DB 80 TCHMDVHFHFWADDFISVNTDQSGNYSQCGSFLLAESIKPAPPFNVTTFSGQYNISWR 139
 QY 121 SDYEDPAFYMLKGLQYELQYRNRPWAVSPRKLISVDSRSVSLLPLEFRKDSSEYELQ 180
 DB 140 SDYEDPAFYMLKGLQYELQYRNRPWAVSPRKLISVDSRSVSLLPLEFRKDSSEYELQ 199
 QY 181 VRAGPMGSSYQGTWSEWSDPVIFQTSBELKEGWNPH 218
 DB 200 VRAGPMGSSYQGTWSEWSDPVIFQTSBELKEGWNPH 237

RESULT 3

AAY69883

ID AAY69883 standard; protein; 361 AA.

XX AAY69883;

XX 24-MAY-2000 (first entry)

XX Human haemopoietin receptor family member NR8alpha.

XX Haemopoietin receptor family; NR8; antibody; diagnosis;
 XX blood formation disorder.

XX Homo sapiens.

XX WO9967290-A1.

XX 29-DEC-1999.

XX 23-JUN-1999; 99WO-JP003351.

XX 24-JUN-1998; 98JP-00214720.

XX 19-OCT-1998; 98JP-00297409.

XX (CHUS) CHUGAI RES INST MOLECULAR MEDICINE INC.

XX Nomura H, Maeda M;

XX WPI; 2000-116933/10.

XX N-PSDB; AAZ59237.

XX Hemopoietin receptor protein family NR8 used for diagnosis of blood
 PT formation disorders.
 XX
 XX Claim 1; Fig 5-6; 176pp; Japanese.
 XX
 CC This sequence represents a novel haemopoietin receptor protein family
 CC NR8, designated NR8alpha. Antibodies to the NR8 family proteins are used
 CC for the diagnosis of blood formation disorders. Compounds identified as
 CC binding to the proteins are used for the treatment of such disorders
 XX
 XX Sequence 361 AA;
 Query Match 100.0%; Score 1195; DB 3; Length 361;
 Best Local Similarity 100.0%; Pred. No. 8.9e-115; Indels 0; Gaps 0;
 Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CPDLVCYTDYLTQVICILEMNLHPSLTTLTWQDYELKDEATCSLHRSANATHATY 60
 DB 20 CPDLVCYTDYLTQVICILEMNLHPSLTTLTWQDYELKDEATCSLHRSANATHATY 79
 QY 61 TCHMDVHFHMADDIFSVNITDQSGNYSQECGSLLAESIKPAPPFNVTVPFSGQYNISWR 120
 DB 80 TCHMDVHFHMADDIFSVNITDQSGNYSQECGSLLAESIKPAPPFNVTVPFSGQYNISWR 139
 QY 121 SDYEDPAFVLMKGLQYELQYENRGDPWAVSPRKLISVDSRSVSLLPLEFRKDSYELQ 180
 DB 140 SDYEDPAFVLMKGLQYELQYENRGDPWAVSPRKLISVDSRSVSLLPLEFRKDSYELQ 199
 QY 181 VRAGMPGSSYQGTWSESDPVIPTQSEELKEGWNPH 218
 DB 200 VRAGMPGSSYQGTWSESDPVIPTQSEELKEGWNPH 237
 RESULT 4
 ID AAY27450
 AC AAY27450;
 DT 26-NOV-1999 (first entry)
 DE Human MU-1 hematopoietin receptor protein.
 XX
 KW MU-1 hematopoietin receptor protein; e MU-1 protein; gene therapy;
 KW cell proliferation; cytokine production; immune response; cancer;
 KW autoimmune disease; transplant rejection; hematopoiesis; anemia;
 KW gene mapping; nutritional supplement; human.
 XX
 OS Homo sapiens.
 XX
 FN WO9947675-A1.
 XX
 PD 23-SEP-1999.
 XX
 PF 17-MAR-1999; 99WO-US005854.
 XX
 PR 17-MAR-1998; 98US-00040005.
 XX
 XX (GENY) GENETICS INST INC.
 XX
 PA Donaldson D, Ungar M;
 PI
 PI WPI: 1999-562115/47.
 DR N-PSDB; AA207535.
 DR
 XX New nucleic acid encoding the MU-1 hematopoietin receptor protein, used
 PT for treating e.g. cancer, autoimmune disease or abnormal hematopoiesis.
 XX
 PS Claim 9; Page 33-35; 37pp; English.
 CC
 CC This represents a MU-1 hematopoietin receptor protein. The protein can be
 CC produced by standard recombinant methodology. The MU-1 protein has the

CC biological activity of the MU-1 hematopoietin receptor superfamily chain.
 It is used to screen for specific binding agents; to raise specific
 CC antibodies; as assay reagents, tissue markers etc. and therapeutically
 CC (optionally expressed from the MU-1 gene by gene therapy). Many possible
 CC activities/uses of the MU-1 protein are described without supporting
 CC evidence, e.g. they regulate cell proliferation and differentiation,
 CC induce production of cytokines, stimulate or suppress an immune response
 CC (e.g. for treating immune deficiency of any etiology, cancer or
 CC autoimmune disease, and for preventing transplant rejection) and regulate
 CC of hematopoiesis, e.g. for treating anemia. The MU-1 gene is used as a
 CC research reagent, for recombinant production of the protein, as tissue or
 CC molecular weight marker, for gene mapping; for production of anti-DNA or
 CC anti-protein antibodies etc. The MU-1 protein and the nucleic acids are
 CC also useful as nutritional supplements or sources and the antibodies can
 CC be used therapeutically, as assay reagents and for affinity purification
 XX
 XX Sequence 538 AA;
 Query Match 100.0%; Score 1195; DB 2; Length 538;
 Best Local Similarity 100.0%; Pred. No. 1.6e-114;
 Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CPDLVCYTDYLTQVICILEMNLHPSLTTLTWQDYELKDEATCSLHRSANATHATY 60
 DB 20 CPDLVCYTDYLTQVICILEMNLHPSLTTLTWQDYELKDEATCSLHRSANATHATY 79
 QY 61 TCHMDVHFHMADDIFSVNITDQSGNYSQECGSLLAESIKPAPPFNVTVPFSGQYNISWR 120
 DB 80 TCHMDVHFHMADDIFSVNITDQSGNYSQECGSLLAESIKPAPPFNVTVPFSGQYNISWR 139
 QY 121 SDYEDPAFVLMKGLQYELQYENRGDPWAVSPRKLISVDSRSVSLLPLEFRKDSYELQ 180
 DB 140 SDYEDPAFVLMKGLQYELQYENRGDPWAVSPRKLISVDSRSVSLLPLEFRKDSYELQ 199
 QY 181 VRAGMPGSSYQGTWSESDPVIPTQSEELKEGWNPH 218
 DB 200 VRAGMPGSSYQGTWSESDPVIPTQSEELKEGWNPH 237
 RESULT 5
 ID AAB18634
 AC AAB18634 standard; protein; 538 AA.
 XX
 AC AAB18634;
 XX
 DT 22-JAN-2001 (first entry)
 XX
 DE A human zalphall ligand polypeptide.
 XX
 KW zalphall ligand; cytokine; haematopoietic cell proliferation; lymphoma;
 KW tumorigenesis; leukaemia; hematopoiesis; B cell tumour.
 XX
 OS Homo sapiens.
 XX
 FN WO2000053761-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 09-MAR-2000; 2000WO-US006067.
 XX
 PR 09-MAR-1999; 99US-00264908.
 PR 11-MAR-1999; 99US-00265992.
 PR 01-JUL-1999; 99US-0142013P.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 XX
 XX Novak JB, Presnell SR, Sprecher CA, Foster DC, Holly RD;
 PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
 XX
 XX WPI: 2000-565600/52.
 DR N-PSDB; AAA75557.
 DR
 XX New human cytokine, designated zalphall ligand, useful for stimulating

PT the proliferation and/or development of hematopoietic cells in vitro and
 PT in vivo, and for treating tumorigenesis.

PS Disclosure; Page 255-256; 256pp; English.

XX The present sequence represents a human zalphall ligand polypeptide,
 CC which is a cytokine. The zalphall ligand is useful for stimulating the
 CC proliferation and development of hematopoietic cells in vitro and in
 CC vivo. Zalphall ligand polynucleotides can be used as primers or probes
 CC for cloning the zalphall gene. The zalphall ligand is useful for treating
 CC tumorigenesis. A zalphall ligand-saporin fusion toxin may be used for
 CC treating leukaemia and lymphomas. Antagonists against zalphall ligand
 CC are useful as research reagents for characterizing ligand-receptor
 CC interaction. Antagonists are also useful for inhibiting expansion,
 CC proliferation, activation and differentiation of cells involved in
 CC regulating hematopoiesis. The zalphall ligand may also be used to
 CC stimulate an immune response against B cell tumour, a virus, a parasite
 CC or a bacterium. The zalphall polypeptides, polynucleotides, antagonists,
 CC agonists and antibodies are also useful for the detection, diagnosis,
 CC prevention, and treatment of diseases associated with a zalphall ligand
 CC genetic defect

XX Sequence 538 AA;

Query Match 100.0%; Score 1195; DB 3; Length 538;
 Best Local Similarity 100.0%; Pred. No. 1.6e-114;
 Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCTDYLTQVICILEMNLHPSTLTITWQDQYEELKDEATSCSLHRSAHNATHATY 60
 DB 20 CPDLVCTDYLTQVICILEMNLHPSTLTITWQDQYEELKDEATSCSLHRSAHNATHATY 79
 QY 61 TCHMDVFHFMAADIFSVNITDQSGNYSQCGSFLLAESIKPAPPFNVTTFSGQYNISWR 120
 DB 80 TCHMDVFHFMAADIFSVNITDQSGNYSQCGSFLLAESIKPAPPFNVTTFSGQYNISWR 139
 QY 121 SDYEDPAFYMLKGLQYELQYRNRGDPWAVSPRRKLIISVDSRSVLLPLEFRKDSSEYELQ 180
 DB 140 SDYEDPAFYMLKGLQYELQYRNRGDPWAVSPRRKLIISVDSRSVLLPLEFRKDSSEYELQ 199
 QY 181 VRAGPMFGSSYQGTWSESDPVIQTQSEBELKEGWNPH 218
 DB 200 VRAGPMFGSSYQGTWSESDPVIQTQSEBELKEGWNPH 237

RESULT 6

AA45031
 ID AAY45031 standard; protein; 538 AA.

XX AAY45031;

XX 31-MAY-2000 (first entry)

DE HUMAN Orphan Cytokine Receptor 10 (OCR10)-A polypeptide.

XX Human; Orphan Cytokine Receptor 10-A; OCR10-A; cytokine; screen;
 XX cognate ligand; treatment; endocrine disorder; immune disorder.

XX Homo sapiens.

XX WO200008152-A1.

XX 17-FEB-2000.

XX 16-JUL-1999; 99WO-US016060.

XX 04-AUG-1998; 98US-00128820.

XX (REGE-) REGENERON PHARM INC.

XX Maslakowski PJ, Morris J, Valenzuela DM;

XX WPI; 2000-205707/18.

DR N-PSDB; AAZ50748.

XX New HUMAN orphan cytokine receptors 10 and 10-A useful for screening for
 PT drugs e.g. receptor agonists that may mediate survival and
 PT differentiation in cells naturally expressing the receptor and for
 PT screening for cognate ligands.

XX Example 10; Page 39-41; 54pp; English.

XX The present sequence is that of HUMAN Orphan Cytokine Receptor 10-A
 CC (OCR10-A) polypeptide. It is expressed at high levels in spleen, thymus,
 CC peripheral blood leucocytes and lymph nodes and moderately in heart and
 CC placenta. It has a role in immune system and cytokine function. It is
 CC useful in screening for cognate ligands or drugs that mediate survival
 CC and differentiation of cells expressing this receptor. Modified HUMAN
 CC OCR10-A or its agonist can be used in the treatment of endocrine or
 CC immune disorders

XX Sequence 538 AA;

Query Match 100.0%; Score 1195; DB 3; Length 538;
 Best Local Similarity 100.0%; Pred. No. 1.6e-114;
 Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCTDYLTQVICILEMNLHPSTLTITWQDQYEELKDEATSCSLHRSAHNATHATY 60
 DB 20 CPDLVCTDYLTQVICILEMNLHPSTLTITWQDQYEELKDEATSCSLHRSAHNATHATY 79
 QY 61 TCHMDVFHFMAADIFSVNITDQSGNYSQCGSFLLAESIKPAPPFNVTTFSGQYNISWR 120
 DB 80 TCHMDVFHFMAADIFSVNITDQSGNYSQCGSFLLAESIKPAPPFNVTTFSGQYNISWR 139
 QY 121 SDYEDPAFYMLKGLQYELQYRNRGDPWAVSPRRKLIISVDSRSVLLPLEFRKDSSEYELQ 180
 DB 140 SDYEDPAFYMLKGLQYELQYRNRGDPWAVSPRRKLIISVDSRSVLLPLEFRKDSSEYELQ 199
 QY 181 VRAGPMFGSSYQGTWSESDPVIQTQSEBELKEGWNPH 218
 DB 200 VRAGPMFGSSYQGTWSESDPVIQTQSEBELKEGWNPH 237

RESULT 7

AA45986

ID AAY69886 standard; protein; 538 AA.

XX AAY69886;

XX 24-MAY-2000 (first entry)

DE Human haemopoietin receptor family member NR8gamma.

XX Haemopoietin receptor family; NR8; antibody; diagnosis;
 XX blood formation disorder.

XX Homo sapiens.

XX WO9967290-A1.

XX 29-DEC-1999.

XX 23-JUN-1999; 99WO-JP003351.

XX 24-JUN-1998; 98JP-00214720.

XX 19-OCT-1998; 98JP-00297409.

XX (CHUS) CHUGAI RES INST MOLECULAR MEDICINE INC.

XX Nomura H, Maeda M;

XX WPI; 2000-116933/10.

XX N-PSDB; AAZ59240.

XX Hemopoietin receptor protein family NR8 used for diagnosis of blood

PT formation disorders.
XX
PS Claim 4; Fig 9-10; 176pp; Japanese.
XX
CC This sequence represents a novel haemopoietin receptor protein family
CC NR8, designated NR8gamma. Antibodies to the NR8 family proteins are used
CC for the diagnosis of blood formation disorders. Compounds identified as
CC binding to the proteins are used for the treatment of such disorders
XX
SQ Sequence 538 AA;

Query Match 100.0%; Score 1195; DB 3; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.6e-114;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCTDYLTQVTCILEMNLHPSTLTWTQDQYELKDEATSCSLHRSAAHATHATY 60
Db 20 CPDLVCTDYLTQVTCILEMNLHPSTLTWTQDQYELKDEATSCSLHRSAAHATHATY 79
QY 61 TCHMDVFFHMADDFISVNTDQSGNYSQECGFLAESIKPAPPFNVTVTFSGQYNISWR 120
Db 80 TCHMDVFFHMADDFISVNTDQSGNYSQECGFLAESIKPAPPFNVTVTFSGQYNISWR 139
QY 121 SDYEDPAFYMKGKQLQYELQYRNRGDPWAVSPRKLISVDSRSVSLPLLEPRKDSYELQ 180
Db 140 SDYEDPAFYMKGKQLQYELQYRNRGDPWAVSPRKLISVDSRSVSLPLLEPRKDSYELQ 199
QY 181 VRAGPMFGSSVQGTWSESDPVIPTQSEELKEGWNPH 218
Db 200 VRAGPMFGSSVQGTWSESDPVIPTQSEELKEGWNPH 237

RESULT 8
AAV79312
ID AAV79312 standard; protein; 538 AA.
XX
AC AAV79312;
XX
DT 18-JUL-2000 (first entry)
XX
DE Human cytokine receptor zalphall.
XX
KW Cytokine receptor; zalphall; human; chromosome 16p11.1; apoptosis;
KW signal transduction; growth factor; cancer; tumour; infection;
KW immunosuppressive; immunostimulant; autoimmune disease; leukaemia;
KW lymphoma; transplant rejection; therapy; diagnosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 1..19
FT Peptide /note= "signal peptide"
FT Protein 20..538
FT /note= "mature protein; a polypeptide comprising the
FT mature protein is specifically claimed in Claim 27(d)"
FT Domain 20..237
FT /note= "cytokine-binding domain; a polypeptide comprising
FT this domain is specifically claimed in Claim 27(a)"
FT Domain 192..202
FT /note= "penultimate strand region"
FT Region 214..218
FT /note= "WSXWS motif"
FT Domain 238..255
FT /note= "transmembrane domain"
FT Domain 256..538
FT /note= "intracellular signalling domain; a polypeptide
FT comprising this domain is specifically claimed in Claim
FT 27(c)"
FT Region 267..273
FT /note= "Box I signalling site"
FT Region 301..304
FT /note= "Box II signalling site"
XX

PN WO200017235-A2.
XX
PD 30-MAR-2000.
XX
XX 23-SEP-1999; 99WO-US022149.
XX
XX 23-SEP-1998; 98US-00159254.
PR 09-MAR-1999; 99US-00285117.
PR 06-JUL-1999; 99US-00347930.
XX
XX (ZYMO) ZYMOGENETICS INC.
PA
PR Presnell SR, Conklin DC, Novak JE, Hammond AK;
XX
XX WPI: 2000-292825/25.
DR N-PSDB; AA294533; AA294534.
XX
XX Novel nucleic acid encoding zalphall polypeptide, useful for treating
PT e.g. viral infection or tumors, and for identifying ligands that
PT stimulate cell proliferation.
XX
PS Claim 27(e); Page 148-149; 190pp; English.
XX
XX The present sequence is that of zalphall, a novel human class I cytokine
CC receptor that may be involved in an apoptotic cellular pathway, or is a
CC cell signalling molecule, growth factor receptor, or extracellular
CC matrix associated protein with growth factor hormone activity. The
CC sequence was deduced from a cDNA clone (see AA294533) isolated from a
CC spinal cord library. Polypeptides comprising amino acids 20-237, 20-255,
CC 256-538, 20-538 and 1-538 of the present sequence are claimed. Zalphall
CC is expressed in lymph node, peripheral blood leucocytes, spleen and
CC thymus. The mRNA is also abundant in the Raji cell line (ATCC CCL 86)
CC derived from Burkitt's lymphoma. Zalphall polypeptides, and fusion
CC proteins including them, can be obtained by expression in recombinant
CC host cells. They are used: to detect ligands (also ligand agonists and
CC antagonists) that stimulate proliferation and/or development of
CC haematopoietic, lymphoid and myeloid cells, in vitro or in vivo, e.g. as
CC a replacement for serum in culture media; in soluble form to block ligand
CC activity (direct antagonists) and to detect ligand-expressing cancers; to
CC raise specific antibodies; and for purification of cognate ligands.
CC Agonistic ligands may stimulate cell-mediated immunity, e.g. for treating
CC (viral) infections associated with immunosuppression, improving the
CC activity of vaccines, suppressing tumours, treating leukaemia and
CC improving T-cell regeneration after bone marrow transplant. Antagonists
CC are useful as immunosuppressants, e.g. in the treatment of autoimmune
CC disease (e.g. rheumatoid arthritis, multiple sclerosis, diabetes), to
CC prevent transplant rejection and to treat T-cell leukemia or lymphoma
XX
XX Sequence 538 AA;
SQ

Query Match 100.0%; Score 1195; DB 3; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.6e-114;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCTDYLTQVTCILEMNLHPSTLTWTQDQYELKDEATSCSLHRSAAHATHATY 60
Db 20 CPDLVCTDYLTQVTCILEMNLHPSTLTWTQDQYELKDEATSCSLHRSAAHATHATY 79
QY 61 TCHMDVFFHMADDFISVNTDQSGNYSQECGFLAESIKPAPPFNVTVTFSGQYNISWR 120
Db 80 TCHMDVFFHMADDFISVNTDQSGNYSQECGFLAESIKPAPPFNVTVTFSGQYNISWR 139
QY 121 SDYEDPAFYMKGKQLQYELQYRNRGDPWAVSPRKLISVDSRSVSLPLLEPRKDSYELQ 180
Db 140 SDYEDPAFYMKGKQLQYELQYRNRGDPWAVSPRKLISVDSRSVSLPLLEPRKDSYELQ 199
QY 181 VRAGPMFGSSVQGTWSESDPVIPTQSEELKEGWNPH 218
Db 200 VRAGPMFGSSVQGTWSESDPVIPTQSEELKEGWNPH 237

RESULT 9
AAB48001

ID AAB48001 standard; protein; 538 AA.
 AC AAB48001;
 XX 19-MAR-2001 (first entry)
 XX Human IL-9/IL-2 receptor-like 16445 protein.
 XX Interleukin-9; IL-9; IL-2 receptor; 16445 protein; inflammatory;
 KW T-lymphocyte-related disorder; antihistaminic; antiproliferative; human;
 KW immunosuppressive; antiallergic; antidiabetic; antithyroid; cytostatic;
 KW antidiarrheic; nephrotropic; gene therapy.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 PH Peptide 1..19
 FT /note= "signal peptide"
 FT Protein 20..538
 FT /note= "mature protein"
 PN W0200069880-A1.
 XX 23-NOV-2000.
 XX 18-MAY-2000; 2000WO-US013687.
 XX 18-MAY-1999; 99US-00313913.
 XX (MILL-) MILLENNIUM PHARM INC.
 PA Hodge MR;
 PI WPI; 2001-016209/02.
 DR N-PSDB; AAC84147.
 DR Novel interleukin-9/interleukin-2 receptor-like polypeptides useful for
 PT diagnosis and treatment of immune, inflammatory and respiratory disorders
 PT and in screening assays for identifying modulators.
 XX Claim 8; Page 104-106; 119pp; English.
 XX The invention relates to isolated human and murine interleukin-9 (IL-9)
 CC /IL-2 receptor-like polypeptides. The plasmid containing the encoding
 CC cDNA insert is deposited as ATCC PTA-350. The IL-9/IL-2 receptor-like
 CC polypeptides (16445 proteins) can be recombinantly produced using
 CC standard recombinant methodology. The 16445 proteins are used for
 CC identifying their modulators and for diagnosis and treatment of immune,
 CC inflammatory and respiratory disorders and disorders associated with
 CC lungs, colon, kidney and lymphoid tissues including tonsil and thymus, in
 CC particular T-lymphocyte-related disorders including atopic conditions
 CC such as asthma allergy, rheumatoid arthritis, psoriasis, chronic
 CC inflammatory diseases and graft versus host disease, disorders involving
 CC the colon such as diarrhoea, dysentery, infectious enterocolitis, kidney
 CC disorders including poly cystic kidney disease, cystic renal dysplasia,
 CC disorders of the thymus including lymphomas, Hodgkin disease and
 CC carcinoids. The 16445 polypeptides are also useful as modulating agents
 CC in cellular processes including growth promoting activity, particularly
 CC the antigen-independent proliferation of T-helper cell clones. The
 CC encoding nucleic acid is useful as primers or hybridization probes for
 CC the detection of IL-9/IL-2 receptor-like encoding nucleic acids and for
 CC tissue typing and in forensic biology. The present sequence represents
 CC the human IL-9/IL-2 receptor-like polypeptide (AAH16445)
 XX
 SQ Sequence 538 AA;
 Query Match 100.0%; Score 1195; DB 4; Length 538;
 Best Local Similarity 100.0%; Pred. No. 1.6e-114; Indels 0; Gaps 0;
 Matches 216; Conservative 0; Mismatches 0;
 QY 1 CPDLVCYTDYLVICILEMNLHPSTLTITWQDQVEELKDEATSCSLRSANATHATY 60
 DB 20 CPDLVCYTDYLVICILEMNLHPSTLTITWQDQVEELKDEATSCSLRSANATHATY 79

QY 61 TCHMDVHFHMADDIFSVNITDQSGNYSQBCSGFLAESIKPAPPFNVTVPSCQYNISWR 120
 DB 80 TCHMDVHFHMADDIFSVNITDQSGNYSQBCSGFLAESIKPAPPFNVTVPSCQYNISWR 139
 QY 121 SDYEDPAPYMLKGKLYELOVRNRGDPWAVSPRKLISVDNRSLPLLEFRKDSYELQ 180
 DB 140 SDYEDPAPYMLKGKLYELOVRNRGDPWAVSPRKLISVDNRSLPLLEFRKDSYELQ 199
 QY 181 VRAGMPGSSVQGTWSEWSDPVIFQTQSEELKEGWNPH 218
 DB 200 VRAGMPGSSVQGTWSEWSDPVIFQTQSEELKEGWNPH 237

RESULT 10

ABB81960
 ID ABB81960 standard; protein; 538 AA.
 XX ABB81960;
 XX 25-NOV-2002 (first entry)
 XX Human 16445 protein.
 XX Interleukin; IL-9; IL-2; 16445; antiallergic; antiproliferative; human;
 KW antiproliferative; antiallergic; immunosuppressive; cytostatic; virucide;
 KW antirheumatic; antihistaminic; antidiabetic; antithyroid; dermatological;
 KW nephrotropic; antibacterial; tuberculostatic; antileptotic; antipyrretic;
 KW antitumor; gene therapy; receptor.
 XX Homo sapiens.
 XX US2002090680-A1.
 XX 11-JUL-2002.
 XX 26-SEP-2001; 2001US-00965313.
 XX 18-MAY-1999; 99US-00313913.
 XX 18-MAY-2000; 2000US-00574100.
 XX (MILL-) MILLENNIUM PHARM INC.
 Hodge MR;
 WPI; 2002-655832/70.
 N-PSDB; ABQ79536.
 New interleukin-9/interleukin-2 receptor-like polypeptides and
 polynucleotides for diagnosing, treating respiratory, T-lymphocyte
 related disorders and disorders associated with lung, colon, kidney and
 lymphoid tissues.

Claim 8; Page 31-33; 54pp; English.

The invention relates to isolated interleukin (IL)-9/IL-2 receptor-like
 polypeptide, 16445. The 16445 polypeptides can be expressed by standard
 recombinant methodology. The 16445 polypeptide, polynucleotides and their
 modulators are useful for modulating the immune, inflammatory and
 respiratory responses, for the diagnosis and treatment of immune and
 respiratory disorders, particularly for the treatment and diagnosis of T-
 lymphocyte-related disorders, including, atopic conditions, such as
 asthma and allergy, including allergic rhinitis, psoriasis, the effects
 of pathogen infection, chronic inflammatory diseases, organ-specific
 autoimmunity, graft rejection, and graft versus host disease. The
 molecules are also useful as modulating agents in a variety of cellular
 processes including growth promoting activity, particularly the antigen
 independent proliferation of T-helper cell clones, and direct effects on
 normal haemopoietic progenitors, human T cells, B cells, thymocytes,
 thymic lymphomas and neuronal cell lines. They are useful for the
 modulation, diagnosis, and treatment of immune, inflammatory, and
 respiratory disorders and disorders associated with lungs, colon, kidney,
 and lymphoid tissues including tonsil and thymus. The present sequence

CC represents a human 16445 polypeptide

XX Sequence 538 AA;

SQ Query Match 100.0%; Score 1195; DB 5; Length 538;

Best Local Similarity 100.0%; Pred. No. 1.6e-114;

Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY 60

Db 20 CPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY 79

QY 61 TCHMDVHFHMADDFISVNTDQSGNSQCGSFLLAESIKPAPPFNVTTFSGQYNISWR 120

Db 80 TCHMDVHFHMADDFISVNTDQSGNSQCGSFLLAESIKPAPPFNVTTFSGQYNISWR 139

QY 121 SYDEDPAFYMLKGLQYELQYRNRPDPAVSPRRKLI SVDSRSVLLPLEFRKDSSEYELQ 180

Db 140 SYDEDPAFYMLKGLQYELQYRNRPDPAVSPRRKLI SVDSRSVLLPLEFRKDSSEYELQ 199

QY 181 VRAGMPGSSYQGTWSESDPVIFQTQSEELKEGWNPH 218

Db 200 VRAGMPGSSYQGTWSESDPVIFQTQSEELKEGWNPH 237

RESULT 11

AAU11912

XX ID AAU11912 standard; protein; 538 AA.

XX AC AAU11912;

XX DT 09-APR-2002 (first entry)

XX DE Human MU-1 haematopoietin receptor superfamily chain protein sequence.

XX KW Human; MU-1; haematopoietin receptor superfamily chain; thyroiditis;

XX KW immune deficiency; anaemia; autoimmune disorder; multiple sclerosis;

XX KW systemic lupus erythematosus; rheumatoid arthritis;

XX KW pulmonary inflammation; insulin dependent diabetes mellitus;

XX KW nutritional supplement; cytokine receptor family.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Domain 237..254

XX FT /note= "Transmembrane domain"

XX PN WO200185792-A2.

XX PD 15-NOV-2001.

XX PF 11-MAY-2001; 2001WO-US015395.

XX PR 05-NOV-1999; 99US-00569384.

XX PA (GENY) GENETICS INST INC.

XX PI Donaldson DD, Unger MJ, Young DA, Whitters MJ, Lowe L, Collins M;

XX DR WPI: 2002-062239/08.

XX DR N-PSDB; AAS17248.

XX PS New polypeptide, useful for identifying compounds binding to MU-1, and

XX PS for treating multiple sclerosis, rheumatoid arthritis, diabetes and

XX PS asthma, comprises the isolated murine MU-1 protein, and a hematopoietin

XX PS receptor superfamily chain.

XX PS Disclosure; Fig 4; 59pp; English.

XX CC The present invention relates to a new murine MU-1 protein, a

XX CC haematopoietin receptor superfamily chain, comprising a fully defined

XX CC sequence of 529 amino acids (AAU1915) as given in the specifications or

CC invention may exhibit cytokine, cell proliferation or cell

CC differentiation activity and may also exhibit immune stimulating or

CC immune suppressing activity and can be useful in the treatment of various

CC immune deficiencies and disorders including severe combined

CC immunodeficiency (SCID). Another use of the invention is treating

CC autoimmune disorders such as connective tissue disease, multiple

CC sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune

CC pulmonary inflammation, autoimmune thyroiditis, insulin dependent

CC diabetes mellitus, and autoimmune inflammatory eye disease. The invention

CC is useful for the treatment of myeloid or lymphoid cell deficiencies and

CC in treating various anemias or for use in conjunction with

CC irradiation/chemotherapy to stimulate the production of erythroid

CC precursors and/or erythroid cells. The polynucleotides and proteins can

CC also be used as nutritional sources or supplements. The present protein

CC sequence represents the human MU-1 haematopoietin receptor superfamily

CC chain. MU-1 is also a member of the cytokine receptor family. This

CC sequence was used in the invention for the characterisation of previously

CC unknown members of the haematopoietin receptor superfamily

XX

SQ Sequence 538 AA;

Query Match 100.0%; Score 1195; DB 5; Length 538;

Best Local Similarity 100.0%; Pred. No. 1.6e-114;

Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY 60

Db 20 CPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY 79

QY 61 TCHMDVHFHMADDFISVNTDQSGNSQCGSFLLAESIKPAPPFNVTTFSGQYNISWR 120

Db 80 TCHMDVHFHMADDFISVNTDQSGNSQCGSFLLAESIKPAPPFNVTTFSGQYNISWR 139

QY 121 SYDEDPAFYMLKGLQYELQYRNRPDPAVSPRRKLI SVDSRSVLLPLEFRKDSSEYELQ 180

Db 140 SYDEDPAFYMLKGLQYELQYRNRPDPAVSPRRKLI SVDSRSVLLPLEFRKDSSEYELQ 199

QY 181 VRAGMPGSSYQGTWSESDPVIFQTQSEELKEGWNPH 218

Db 200 VRAGMPGSSYQGTWSESDPVIFQTQSEELKEGWNPH 237

RESULT 12

AAE13726

XX ID AAE13726 standard; protein; 538 AA.

XX AC AAE13726;

XX DT 26-FEB-2002 (first entry)

XX DE Human soluble Zalphall cytokine receptor protein.

XX KW Human; Zalphall; cytokine receptor; immunosuppressive; cytostatic;

XX KW inflammatory disorder; haemostatic; cell proliferation; immune disorder;

XX KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;

XX KW myasthenia gravis; systemic lupus erythematosus; SLE; diabetes; asthma;

XX KW ulcerative colitis; inflammatory bowel disease; Crohn's disease; sepsis;

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Peptide 1..19

XX FT /label= Signal_peptide

XX FT Protein 20..538

XX FT /label= Mature_Zalphall_protein

XX FT Domain 20..237

XX FT /label= Cytokine_binding_domain

XX FT Domain 120..123

XX FT /label= Domain_linker

XX FT Region 192..202

XX FT /notes= "Perultimate strand region"

XX FT Domain 214..218

FT Domain /note= "WSXWS motif"
 FT 238. 255
 FT /label= Transmembrane_domain
 FT Domain 256. .538
 FT /label= Intracellular_signalling_domain
 FT Region 267. .273
 FT /note= "Box I signalling site"
 FT Region 301. .304
 FT /note= "Box II signalling site"
 FT Binding-site 519. 522
 FT /label= STAR3_binding_site
 XX W020017171-A2.
 PN XX
 PD 18-OCT-2001.
 XX
 XX 03-APR-2001; 2001WC-US010872.
 XX
 XX 05-APR-2000; 2000US-0194731P.
 PR 28-JUL-2000; 2000US-0222121P.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 PA
 XX Sprecher CA, Novak JE, West JW, Presnell SR, Holly RD, Nelson AJ;
 PI WPI; 2002-025898/03.
 XX N-PSDB; AAD22918.
 DR
 DR Novel soluble receptor polypeptides and polynucleotides used as cytokine
 PT antagonist for stimulating ligand activity-induced proliferation of
 PT hematopoietic cells and for suppressing immune response in a mammal.
 PT
 PS Example 1; Page 172-173; 243pp; English.
 XX
 CC The invention relates to an isolated soluble zalphall cytokine receptor
 CC polypeptide and their cDNA molecules. Zalpha proteins are useful for
 CC inhibiting or antagonising the ligand activity-induced proliferation of
 CC haematopoietic cells and haematopoietic cell progenitors preferably
 CC lymphoid cells which are natural killer cells or cytotoxic T cells.
 CC Zalpha is useful for treating immune and inflammatory disorders, for
 CC reducing proliferation of neoplastic B or T cells, for suppressing an
 CC immune response in a mammal exposed to an antigen or pathogen. Zalpha is
 CC useful for treating diseases that require immune regulation including
 CC autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,
 CC myasthenia gravis, systemic lupus erythematosus (SLE) and diabetes;
 CC asthma, ulcerative colitis, inflammatory bowel disease, Crohn's disease,
 CC sepsis, viral infection (dengue virus infection) and cancer. The present
 CC sequence is human soluble Zalphall cytokine receptor protein
 XX
 SQ Sequence 538 AA;
 Query Match 100.0%; Score 1195; DB 5; Length 538;
 Best Local Similarity 100.0%; Pred. No. 1.6e-114;
 Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CPDLVCTDYLTQVTCILEMNLHPSTLTITWQOQEELKDEATSCSLHRSANATHATY 60
 DB 20 CPDLVCTDYLTQVTCILEMNLHPSTLTITWQOQEELKDEATSCSLHRSANATHATY 79
 QY 61 TCHMDVHFHMADDFISVNIITDQSGNYSQEGCSFLAESIKPAPPFNVTTFSGQYNISWR 120
 DB 80 TCHMDVHFHMADDFISVNIITDQSGNYSQEGCSFLAESIKPAPPFNVTTFSGQYNISWR 139
 QY 121 SDYEDPAPYMLKGKQLQVELQYRNRGDPWAPSPRKLISVDSRSVSLLPLEFRKDSSEYELQ 180
 DB 140 SDYEDPAPYMLKGKQLQVELQYRNRGDPWAPSPRKLISVDSRSVSLLPLEFRKDSSEYELQ 199
 QY 181 VRAGPMFGSSVQGTWSEWSDVIFPQTQSEELKEGNPH 218
 DB 200 VRAGPMFGSSVQGTWSEWSDVIFPQTQSEELKEGNPH 237
 RESULT 13

AAU11978
 ID AAU11978 standard; protein; 538 AA.
 XX
 AC AAU11978;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Human zalphall receptor polypeptide.
 XX
 KW Cytokine; zalphall Ligand; zalphall receptor; NK cell progenitor;
 KW natural killer cell proliferation; T-cell proliferation;
 KW B-cell proliferation; anti-tumour response; immune system;
 KW immunostimulant; cytostatic; human.
 XX
 OS Homo sapiens.
 XX
 XX US6307024-B1.
 XX
 XX 23-OCT-2001.
 XX
 XX 09-MAR-2000; 2000US-00522217.
 PF
 XX 09-MAR-1999; 99US-0123547P.
 PR 11-MAR-1999; 99US-0123904P.
 PR 01-JUL-1999; 99US-0142013P.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 XX
 XX Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
 PI Gross JA, Johnston JW, Nelson AJ, Dillon SR, Hammond AK;
 XX WPI; 2002-040208/05.
 DR N-PSDB; AAS20642.
 XX
 XX New zalphall ligand polypeptides and polynucleotides, useful for
 PT stimulating proliferation, activation, differentiation and/or induction
 PT of inhibition of specialized cell function, or for stimulating an
 PT antigenic response.
 XX
 PS Claim 1; Col 191-194; 105pp; English.
 XX
 CC The present invention relates to the isolation of a novel cytokine,
 CC zalphall ligand and the polynucleotide encoding it. The invention also
 CC gives the sequence for the zalphall receptor and the polynucleotide
 CC encoding it. The zalphall ligand polypeptide stimulates proliferation of
 CC natural killer (NK) cells or NK cell progenitors, the activation of NK
 CC cells, proliferation of T-cells, proliferation of B-cells stimulated with
 CC anti-CD40 antibodies, stimulates an antigenic response in a mammal, and
 CC reduces proliferation of B-cells stimulated with anti-IgM antibodies. The
 CC zalphall ligand polypeptide is also useful in preparing antibodies that
 CC bind to zalphall Ligand epitopes. The zalphall Ligand polynucleotides can
 CC be used as probes or primers to clone regions of a zalphall Ligand gene,
 CC and in gene therapy. Zalphall Ligand may also be used to identify
 CC inhibitors of its activity, to enhance the generation of anti-tumour
 CC responses with or without the infusion of donor lymphocytes, and to
 CC activate or stimulate the immune system. The present sequence represents
 CC human zalphall receptor polypeptide
 XX
 SQ Sequence 538 AA;
 Query Match 100.0%; Score 1195; DB 5; Length 538;
 Best Local Similarity 100.0%; Pred. No. 1.6e-114;
 Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CPDLVCTDYLTQVTCILEMNLHPSTLTITWQOQEELKDEATSCSLHRSANATHATY 60
 DB 20 CPDLVCTDYLTQVTCILEMNLHPSTLTITWQOQEELKDEATSCSLHRSANATHATY 79
 QY 61 TCHMDVHFHMADDFISVNIITDQSGNYSQEGCSFLAESIKPAPPFNVTTFSGQYNISWR 120
 DB 80 TCHMDVHFHMADDFISVNIITDQSGNYSQEGCSFLAESIKPAPPFNVTTFSGQYNISWR 139
 QY 121 SDYEDPAPYMLKGKQLQVELQYRNRGDPWAPSPRKLISVDSRSVSLLPLEFRKDSSEYELQ 180

Db 140 SYEDPAFYMLKGLQYELQYRNRPDPWAVSPRRKLIISVDSRSVLLPLEFRKDSSEYELQ 199
 QY 181 VRAGPMPGSSYQGTWSESDPVIFQTSSEELKEGWNPH 218
 Db 200 VRAGPMPGSSYQGTWSESDPVIFQTSSEELKEGWNPH 237

RESULT 14
 ABR61402
 ID ABR61402 standard; protein; 538 AA.
 XX
 AC ABR61402;
 DT 12-AUG-2003 (first entry)
 XX
 DE Human IL-21R SEQ ID NO:2.
 XX
 KW arthritic disorder; interleukin-21; IL-21; IL-21 receptor; IL-21R;
 KW immune cell activity; cancer; infectious disorder; antirheumatic;
 KW antiarthritic; osteopathic; antiposrotic; cytostatic; antibacterial;
 KW virucide; antiparasitic; immunosuppressive; antidiabetic; dermatological;
 KW neuroprotective; antitumor; antiallergic; antianaemic; hepatotropic;
 KW antithyroid; antinflammatory; immune response; immune disorder;
 KW autoimmune disease; human.
 XX
 OS Homo sapiens.
 XX
 PN WC2003028630-A2.
 XX
 PD 10-APR-2003.
 XX
 PF 04-OCT-2002; 2002WO-US029839.
 XX
 PR 04-OCT-2001; 2001US-00972218.
 XX
 PR 17-APR-2002; 2002US-0373746P.
 XX
 PA (AMHP) WYETH.
 XX
 PI Carter L, Whitters MJ, Collins M, Young DA, Larsen G;
 PI Donaldson DD, Lowe LD, Dunussi K, Ma M, Witek JS, Kasasian MT;
 PI Ungar M;
 XX
 DR WPI; 2003-430146/40.
 DR N-PSDB; ACC80861.
 XX
 PT Treating or preventing arthritic disorder, cancer or infectious disorders
 PT in a subject, involves administering a modulator of interleukin-21 or its
 PT receptor which modulate immune cell activity.
 XX
 PS Claim 40; Fig 2B; 176pp; English.

The invention relates to a novel method for treating or preventing an
 arthritic disorder in a subject. The method involves administering to the
 subject an interleukin-21 (IL-21)/IL-21 receptor (IL-21R) antagonist
 optionally in combination with another therapeutic agent, to inhibit or
 reduce immune cell activity in the subject. The method is also useful for
 treating or preventing cancer or an infectious disorder, in a subject, by
 administering IL-21/IL-21R agonist, to increase immune cell activity. The
 method of the invention has antirheumatic, antiarthritic, osteopathic,
 antiparasitic, cytostatic, antibacterial, virucide, antiparasitic,
 immunosuppressive, antidiabetic, neuroprotective, dermatological,
 antitumor, antiasthmatic, antiallergic, antianaemic, hepatotropic,
 antithyroid, and antinflammatory activity. The method is useful for
 treating or preventing an arthritic disorder such as rheumatoid
 arthritis, juvenile rheumatoid arthritis, osteoarthritis, psoriatic
 arthritis or ankylosing spondylitis, and also cancer such as solid
 tumour, soft tissue tumour or metastatic lesion, or an infectious
 disorder such as bacterial, viral or parasitic infection in a mammal,
 preferably human. A method of the invention is also useful for
 increasing the ability of a vaccine composition containing an antigen to
 elicit a protective immune response in a subject against the antigens.
 The antigen is from a pathogen such as virus, bacterium or protozoan, or

CC from cancer or tumour cell antigen, or expressed on the surface of cancer
 CC cell. An alternative method of the invention is useful for modulating the
 CC activity of immune or haematopoietic cells and thus to treat or prevent a
 CC variety of immune disorders, such as autoimmune diseases, for example
 CC diabetes mellitus, multiple sclerosis, myasthenia gravis, systemic lupus
 CC erythematosus, dermatitis, ulcer, asthma, allergic asthma, anaemia,
 CC hepatitis, Graves's disease, graft versus host disease, and scleroderma.
 CC The present sequence is used in an exemplification of the invention
 XX

SQ Sequence 538 AA;

Query Match 100.0%; Score 1195; DB 6; Length 538;
 Best Local Similarity 100.0%; Pred. No. 1.6e-114;
 Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CPDLVCYTDYLVICILEMNLHPSTLTTLTWDQYEEKDEATSCSLRSNAHATHATY 60
 Db 20 CPDLVCYTDYLVICILEMNLHPSTLTTLTWDQYEEKDEATSCSLRSNAHATHATY 79
 Qy 61 TCHMDVPHFWADDIFSVNITDQSGNYSQCGSFLAESIKPAPPFNVTTFSGQYNISWR 120
 Db 80 TCHMDVPHFWADDIFSVNITDQSGNYSQCGSFLAESIKPAPPFNVTTFSGQYNISWR 139
 Qy 121 SYEDPAFYMLKGLQYELQYRNRPDPWAVSPRRKLIISVDSRSVLLPLEFRKDSSEYELQ 180
 Db 140 SYEDPAFYMLKGLQYELQYRNRPDPWAVSPRRKLIISVDSRSVLLPLEFRKDSSEYELQ 199
 Qy 181 VRAGPMPGSSYQGTWSESDPVIFQTSSEELKEGWNPH 218
 Db 200 VRAGPMPGSSYQGTWSESDPVIFQTSSEELKEGWNPH 237

RESULT 15

AAE14939
 ID AAE14939 standard; protein; 538 AA.

XX
 AC AAE14939;

DT 27-AUG-2003 (first entry)

DE Human interleukin-21 (IL-21) receptor.

KW Interleukin-21; antagonist; cancer; inflammatory; autoimmune disorder;
 KW rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus;
 KW myasthenia gravis; diabetes; human; zalfaph receptor; IL-21 receptor.

XX
 OS Homo sapiens.

XX
 PN WC2003040313-A2.

XX
 PD 15-MAY-2003.

XX
 PF 28-OCT-2002; 2002WO-US034502.

XX
 PR 05-NOV-2001; 2001US-0337586P.

XX
 PA (ZYMO) ZYMOGENETICS INC.

XX
 PI Pressnell SR, West JW, Novak JE;

XX
 DR WPI; 2003-441547/41.

XX
 DR N-PSDB; AAD47859.

XX
 PT New IL-21 polypeptide and encoding polynucleotide, useful for diagnosing
 PT and treating disorders with aberrant expression or activity of the IL-21
 PT polypeptide, such as cancer, rheumatoid arthritis, multiple sclerosis and
 PT diabetes.

XX
 PS Example 1; Page 65-67; 71pp; English.

XX
 CC The invention relates to polynucleotides and polypeptides of interleukin-
 CC 21 (IL-21) antagonists, that bind with specificity and exhibit an EG50
 CC that is not detectable in receptor binding studies. The antagonists of

CC the invention have mutations in the D helix of the IL-21 molecule, and
CC can be used to inhibit the activity of IL-21 with its cognate receptor.
CC The IL-21 antagonists are useful for diagnosing and treating disorders
CC involving the aberrant expression or activity of the IL-21 polypeptide,
CC such as cancer, inflammatory and autoimmune disorders, including
CC rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus,
CC myasthenia gravis and diabetes. The polypeptides can also be used to
CC prepare antibodies that bind IL-21 epitopes, peptides or polypeptides,
CC and for enhancing in vivo killing of target tissues. The present sequence
CC is human IL-21 receptor (originally designated zalphall receptor)
XX
SQ

SQ Sequence 538 AA;	
Query Match 100.0%; Score 1195; DB 7; Length 538;	
Best Local Similarity 100.0%; Pred. No. 1.6e-114;	
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 1	CPDLVCYTDYLGQVICILEMWNLHPSTLTITWQDQYEELKDEATCSLHRSAHNATHATY 60
Db 20	CPDLVCYTDYLGQVICILEMWNLHPSTLTITWQDQYEELKDEATCSLHRSAHNATHATY 79
QY 61	TCHMDVHFHMADDFISVNITDQSGNYSCGSGFLLAESIKPAPPFNVTTFSGQYNISWR 120
Db 80	TCHMDVHFHMADDFISVNITDQSGNYSCGSGFLLAESIKPAPPFNVTTFSGQYNISWR 139
QY 121	SDYEDAFYMLKGLQYELQYRNRGDPWAVSPRRKLIISVDSRSVSLPLLEPRKDSSEYELQ 180
Db 140	SDYEDAFYMLKGLQYELQYRNRGDPWAVSPRRKLIISVDSRSVSLPLLEPRKDSSEYELQ 199
QY 181	VRAGPMFGSSYQGTWSEWSDPVIFQTQSEBELKEGWNPH 218
Db 200	VRAGPMFGSSYQGTWSEWSDPVIFQTQSEBELKEGWNPH 237

Search completed: March 3, 2004, 12:35:38
Job time : 53.0065 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1288	100.0	347	1	US-08-052-205-7	Sequence 7, Appli
2	1288	100.0	347	1	US-08-595-974-7	Sequence 7, Appli
3	1288	100.0	369	1	US-08-052-205-4	Sequence 4, Appli
4	1288	100.0	369	1	US-08-595-974-4	Sequence 4, Appli
5	1288	100.0	369	1	US-09-191-786-2	Sequence 2, Appli
6	1288	100.0	691	4	US-09-313-942-20	Sequence 20, Appl
7	1288	100.0	694	4	US-09-313-942-18	Sequence 18, Appl
8	1288	100.0	694	4	US-09-313-942-22	Sequence 22, Appl
9	1282	99.5	482	4	US-09-189-139-2	Sequence 2, Appli
10	1277	99.1	230	1	US-08-052-205-11	Sequence 11, Appl
11	1277	99.1	230	1	US-08-595-974-11	Sequence 11, Appl
12	1277	99.1	252	1	US-08-052-205-9	Sequence 9, Appli
13	1277	99.1	252	1	US-08-595-974-9	Sequence 9, Appli
14	853.5	66.3	369	2	US-08-424-224-2	Sequence 2, Appli
15	853.5	66.3	369	5	PCR-US94-02891-69	Sequence 69, Appl
16	207	16.1	380	1	US-08-609-572-4	Sequence 4, Appli
17	207	16.1	380	3	US-08-841-751-4	Sequence 4, Appli
18	207	16.1	380	3	US-08-846-340-4	Sequence 4, Appli
19	207	16.1	380	3	US-08-846-344-4	Sequence 4, Appli
20	207	16.1	380	4	US-09-301-808-4	Sequence 4, Appli
21	199.5	15.5	383	1	US-08-609-572-2	Sequence 2, Appli
22	199.5	15.5	383	3	US-08-841-751-2	Sequence 2, Appli
23	199.5	15.5	383	3	US-08-846-340-2	Sequence 2, Appli
24	199.5	15.5	383	3	US-08-846-344-2	Sequence 2, Appli
25	199.5	15.5	383	4	US-09-301-808-2	Sequence 2, Appli
26	178	13.8	427	3	US-08-969-125-9	Sequence 9, Appli
27	178	13.8	784	4	US-09-313-942-30	Sequence 30, Appl

Query Match 100.0%; Score 1288; DB 1; Length 347;
Best Local Similarity 100.0%; Pred. No. 1.4e-118;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTTILTPNGEDTTADFFLTMTPTDLSVSTPLPVEQCFVFNVEYMNCTWNSSEPPQ 60
DB 1 LNTTILTPNGEDTTADFFLTMTPTDLSVSTPLPVEQCFVFNVEYMNCTWNSSEPPQ 60

QY 61 TNLTHYWKNSDNDKVKCKSHYLFSEETSCQLOKKEIHLVQYRTDWDHSHTEQSV 120
DB 61 TNLTHYWKNSDNDKVKCKSHYLFSEETSCQLOKKEIHLVQYRTDWDHSHTEQSV 120

QY 121 TQMLKQLNVLIPWAPENLTLHKLSEQLNWNRFNLHCLHLEHLVQYRTDWDHSHTEQSV 180
DB 121 TQMLKQLNVLIPWAPENLTLHKLSEQLNWNRFNLHCLHLEHLVQYRTDWDHSHTEQSV 180

QY 181 DYRHKFSLSVDGQKRYTFRVRSRNPFCGSAQHSWSEHPHWSNTSKEN 232
DB 181 DYRHKFSLSVDGQKRYTFRVRSRNPFCGSAQHSWSEHPHWSNTSKEN 232

RESULT 2
US-08-595-974-7
; Sequence 7, Application US/08595974
; Patent No. 5705608
; GENERAL INFORMATION:
; APPLICANT: SUGAMURA, KAZUO
; APPLICANT: TAKESHITA, TOSHIKAZU
; APPLICANT: ASAO, HIRONOBU
; APPLICANT: NAKAMURA, MASATAKA
; APPLICANT: SHIMAMURA, TOSHIRO
; APPLICANT: SUZUKI, MANABU
; APPLICANT: HAMURO, JUNJI
; TITLE OF INVENTION: HUMAN IL-2 RECEPTOR GAMMA CHAIN MOLECULE
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,974
; FILING DATE: 06-FEB-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/052,205
; FILING DATE: 22-APR-1993
; APPLICATION NUMBER: JP 104947/1992
; FILING DATE: 23-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5705608man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-615-0X
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 347 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-595-974-7

Query Match 100.0%; Score 1288; DB 1; Length 347;
Best Local Similarity 100.0%; Pred. No. 1.4e-118;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTTILTPNGEDTTADFFLTMTPTDLSVSTPLPVEQCFVFNVEYMNCTWNSSEPPQ 60
DB 1 LNTTILTPNGEDTTADFFLTMTPTDLSVSTPLPVEQCFVFNVEYMNCTWNSSEPPQ 60

QY 61 TNLTHYWKNSDNDKVKCKSHYLFSEETSCQLOKKEIHLVQYRTDWDHSHTEQSV 120
DB 61 TNLTHYWKNSDNDKVKCKSHYLFSEETSCQLOKKEIHLVQYRTDWDHSHTEQSV 120

QY 121 TQMLKQLNVLIPWAPENLTLHKLSEQLNWNRFNLHCLHLEHLVQYRTDWDHSHTEQSV 180
DB 121 TQMLKQLNVLIPWAPENLTLHKLSEQLNWNRFNLHCLHLEHLVQYRTDWDHSHTEQSV 180

QY 181 DYRHKFSLSVDGQKRYTFRVRSRNPFCGSAQHSWSEHPHWSNTSKEN 232
DB 181 DYRHKFSLSVDGQKRYTFRVRSRNPFCGSAQHSWSEHPHWSNTSKEN 232

RESULT 3
US-08-052-205-4
; Sequence 4, Application US/08052205
; Patent No. 5510259
; GENERAL INFORMATION:
; APPLICANT: SUGAMURA, KAZUO
; APPLICANT: TAKESHITA, TOSHIKAZU
; APPLICANT: ASAO, HIRONOBU
; APPLICANT: NAKAMURA, MASATAKA
; APPLICANT: SHIMAMURA, TOSHIRO
; APPLICANT: SUZUKI, MANABU
; APPLICANT: HAMURO, JUNJI
; TITLE OF INVENTION: HUMAN IL-2 RECEPTOR GAMMA CHAIN MOLECULE
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/052,205
; FILING DATE: 19930422
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 104947/1992
; FILING DATE: 23-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5510259man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-615-0X
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 369 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-052-205-4

Query Match 100.0%; Score 1288; DB 1; Length 369;
Best Local Similarity 100.0%; Pred. No. 1.5e-118;

Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSESPQP 60

Db 23 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSESPQP 82

QY 61 TNLTLHYWYKNSDNDKVKQCSHYLPSSEITSGCOLQKKEIHLVQTFVVOLODPREPRQA 120

Db 83 TNLTLHYWYKNSDNDKVKQCSHYLPSSEITSGCOLQKKEIHLVQTFVVOLODPREPRQA 142

QY 121 TQMLKQLNQLVWPAPENLTLLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTQSV 180

Db 143 TQMLKQLNQLVWPAPENLTLLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTQSV 202

QY 181 DYRHKFSPLPSVDGQKRYTFRVRSRFPNPLCGSAQHSWSESHPIHWSNTSKEN 232

Db 203 DYRHKFSPLPSVDGQKRYTFRVRSRFPNPLCGSAQHSWSESHPIHWSNTSKEN 254

RESULT 4

US-08-595-974-4

; Sequence 4, Application US/08595974

; Patent No. 5705608

; GENERAL INFORMATION:

; APPLICANT: SUGAMURA, KAZUO

; APPLICANT: TAKESHITA, TOSHIKAZU

; APPLICANT: ASAO, HIRONOBU

; APPLICANT: NAKAMURA, MASATAKA

; APPLICANT: SHIMAMURA, TOSHIRO

; APPLICANT: SUZUKI, MANABU

; APPLICANT: HAMURO, JUNJI

; TITLE OF INVENTION: HUMAN IL-2 RECEPTOR GAMMA CHAIN MOLECULE

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,

; ADDRESS: P.C.

; STREET: 1755 S. Jefferson Davis Highway, Suite 400

; CITY: Arlington

; STATE: Virginia

; COUNTRY: U.S.A.

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/595,974

; FILING DATE: 06-FEB-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/052,205

; FILING DATE: 22-APR-1993

; APPLICATION NUMBER: JP 104947/1992

; FILING DATE: 23-APR-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Oblon, No. 5705608man F.

; REGISTRATION NUMBER: 24,618

; REFERENCE/DOCKET NUMBER: 10-615-0X

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 413-3000

; TELEFAX: (703) 413-2220

; TELEX: 248855 OPAT UR

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 369 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-595-974-4

Query Match 100.0%; Score 1288; DB 1; Length 369;

Best Local Similarity 100.0%; Pred. No. 1.5e-118;

Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSESPQP 60

Db 23 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSESPQP 82

QY 61 TNLTLHYWYKNSDNDKVKQCSHYLPSSEITSGCOLQKKEIHLVQTFVVOLODPREPRQA 120

Db 83 TNLTLHYWYKNSDNDKVKQCSHYLPSSEITSGCOLQKKEIHLVQTFVVOLODPREPRQA 142

QY 121 TQMLKQLNQLVWPAPENLTLLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTQSV 180

Db 143 TQMLKQLNQLVWPAPENLTLLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTQSV 202

QY 181 DYRHKFSPLPSVDGQKRYTFRVRSRFPNPLCGSAQHSWSESHPIHWSNTSKEN 232

Db 203 DYRHKFSPLPSVDGQKRYTFRVRSRFPNPLCGSAQHSWSESHPIHWSNTSKEN 254

RESULT 5

US-09-191-786-2

; Sequence 2, Application US/09191786

; Patent No. 6372898

; GENERAL INFORMATION:

; APPLICANT: Cacalano, Nicholas A.

; APPLICANT: Johnston, James A.

; TITLE OF INVENTION: Mammalian Protein Variants and Methods

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DNAX Research Institute

; STREET: 901 California Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94304-1104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/191,786

; FILING DATE: 11-NOV-1998

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Ching, Edwin P.

; REGISTRATION NUMBER: 34,090

; REFERENCE/DOCKET NUMBER: DX0920

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (650) 852-9196

; TELEFAX: (650) 496-1200

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 369 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..1062

US-09-191-786-2

Query Match 100.0%; Score 1288; DB 4; Length 369;

Best Local Similarity 100.0%; Pred. No. 1.5e-118;

Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSESPQP 60

Db 23 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSESPQP 82

QY 61 TNLTLHYWYKNSDNDKVKQCSHYLPSSEITSGCOLQKKEIHLVQTFVVOLODPREPRQA 120

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Db 83 TNLTLHYWYKNSDNDKVKQKSHYLFSEETSGCQLOKKEIHLVQTFVVLQDPRPRQA 142
Qy 121 TOMLKLQNLVWPAPENLTLHLKLSQLELNWNNRFLNHCLEHLVQYRTDWDHWSWTEQSV 180
Db 143 TOMLKLQNLVWPAPENLTLHLKLSQLELNWNNRFLNHCLEHLVQYRTDWDHWSWTEQSV 202
Qy 181 DYRHKFSLSVDGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHWSNTSKEN 232
Db 203 DYRHKFSLSVDGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHWSNTSKEN 254

RESULT 6
US-09-313-942-20
; Sequence 20, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 691
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-20

Query Match 100.0%; Score 1288; DB 4; Length 691;
Best Local Similarity 100.0%; Pred. No. 3.6e-118; Indels 0; Gaps 0;
Matches 232; Conservative 0; Mismatches 0;

Qy 1 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPOP 60
Db 23 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPOP 82
Qy 61 TNLTLHYWYKNSDNDKVKQKSHYLFSEETSGCQLOKKEIHLVQTFVVLQDPRPRQA 120
Db 83 TNLTLHYWYKNSDNDKVKQKSHYLFSEETSGCQLOKKEIHLVQTFVVLQDPRPRQA 142
Qy 121 TOMLKLQNLVWPAPENLTLHLKLSQLELNWNNRFLNHCLEHLVQYRTDWDHWSWTEQSV 180
Db 143 TOMLKLQNLVWPAPENLTLHLKLSQLELNWNNRFLNHCLEHLVQYRTDWDHWSWTEQSV 202
Qy 181 DYRHKFSLSVDGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHWSNTSKEN 232
Db 203 DYRHKFSLSVDGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHWSNTSKEN 254

RESULT 7
US-09-313-942-18
; Sequence 18, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-18

Query Match 100.0%; Score 1288; DB 4; Length 694;
Best Local Similarity 100.0%; Pred. No. 3.6e-118; Indels 0; Gaps 0;
Matches 232; Conservative 0; Mismatches 0;

Qy 1 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPOP 60
Db 23 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPOP 82
Qy 61 TNLTLHYWYKNSDNDKVKQKSHYLFSEETSGCQLOKKEIHLVQTFVVLQDPRPRQA 120
Db 83 TNLTLHYWYKNSDNDKVKQKSHYLFSEETSGCQLOKKEIHLVQTFVVLQDPRPRQA 142
Qy 121 TOMLKLQNLVWPAPENLTLHLKLSQLELNWNNRFLNHCLEHLVQYRTDWDHWSWTEQSV 180
Db 143 TOMLKLQNLVWPAPENLTLHLKLSQLELNWNNRFLNHCLEHLVQYRTDWDHWSWTEQSV 202
Qy 181 DYRHKFSLSVDGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHWSNTSKEN 232
Db 203 DYRHKFSLSVDGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHWSNTSKEN 254

RESULT 8
US-09-313-942-22
; Sequence 22, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-22

Query Match 100.0%; Score 1288; DB 4; Length 694;
Best Local Similarity 100.0%; Pred. No. 3.6e-118; Indels 0; Gaps 0;
Matches 232; Conservative 0; Mismatches 0;

Qy 1 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPOP 60
Db 23 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPOP 82
Qy 61 TNLTLHYWYKNSDNDKVKQKSHYLFSEETSGCQLOKKEIHLVQTFVVLQDPRPRQA 120
Db 83 TNLTLHYWYKNSDNDKVKQKSHYLFSEETSGCQLOKKEIHLVQTFVVLQDPRPRQA 142
Qy 121 TOMLKLQNLVWPAPENLTLHLKLSQLELNWNNRFLNHCLEHLVQYRTDWDHWSWTEQSV 180
Db 143 TOMLKLQNLVWPAPENLTLHLKLSQLELNWNNRFLNHCLEHLVQYRTDWDHWSWTEQSV 202
Qy 181 DYRHKFSLSVDGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHWSNTSKEN 232
Db 203 DYRHKFSLSVDGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHWSNTSKEN 254

RESULT 9
US-09-189-129-2
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```
; SEQ ID NO 18
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-18

Query Match 100.0%; Score 1288; DB 4; Length 694;
Best Local Similarity 100.0%; Pred. No. 3.6e-118; Indels 0; Gaps 0;
Matches 232; Conservative 0; Mismatches 0;

Qy 1 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPOP 60
Db 23 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPOP 82
Qy 61 TNLTLHYWYKNSDNDKVKQKSHYLFSEETSGCQLOKKEIHLVQTFVVLQDPRPRQA 120
Db 83 TNLTLHYWYKNSDNDKVKQKSHYLFSEETSGCQLOKKEIHLVQTFVVLQDPRPRQA 142
Qy 121 TOMLKLQNLVWPAPENLTLHLKLSQLELNWNNRFLNHCLEHLVQYRTDWDHWSWTEQSV 180
Db 143 TOMLKLQNLVWPAPENLTLHLKLSQLELNWNNRFLNHCLEHLVQYRTDWDHWSWTEQSV 202
Qy 181 DYRHKFSLSVDGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHWSNTSKEN 232
Db 203 DYRHKFSLSVDGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHWSNTSKEN 254

RESULT 8
US-09-313-942-22
; Sequence 22, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-22

Query Match 100.0%; Score 1288; DB 4; Length 694;
Best Local Similarity 100.0%; Pred. No. 3.6e-118; Indels 0; Gaps 0;
Matches 232; Conservative 0; Mismatches 0;

Qy 1 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPOP 60
Db 23 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPOP 82
Qy 61 TNLTLHYWYKNSDNDKVKQKSHYLFSEETSGCQLOKKEIHLVQTFVVLQDPRPRQA 120
Db 83 TNLTLHYWYKNSDNDKVKQKSHYLFSEETSGCQLOKKEIHLVQTFVVLQDPRPRQA 142
Qy 121 TOMLKLQNLVWPAPENLTLHLKLSQLELNWNNRFLNHCLEHLVQYRTDWDHWSWTEQSV 180
Db 143 TOMLKLQNLVWPAPENLTLHLKLSQLELNWNNRFLNHCLEHLVQYRTDWDHWSWTEQSV 202
Qy 181 DYRHKFSLSVDGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHWSNTSKEN 232
Db 203 DYRHKFSLSVDGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHWSNTSKEN 254

RESULT 9
US-09-189-129-2
```

Sequence 2, Application US/09189129
Patent No. 6323027
GENERAL INFORMATION:
APPLICANT: Burkly, Linda C
APPLICANT: Benjamin, Christopher D
APPLICANT: Hession, Catherine A
APPLICANT: Whitty, Adrian
TITLE OF INVENTION: COMMON GAMMA CHAIN BLOCKING AGENTS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Biogen, Inc.
STREET: 14 Cambridge Center
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02142
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/189,129
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: A006 PCT CIP
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: 60/017,466
FILING DATE: 10-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kaplan, Warren A.
REGISTRATION NUMBER: 34,199
REFERENCE/DOCKET NUMBER: A006 PCT CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 679-2000
TELEFAX: 617 679-2838
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 482 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL: YES
ANTI-SENSE: NO
US-09-189-129-2

Query Match 99.5%; Score 1282; DB 4; Length 482;
Best Local Similarity 99.6%; Pred. No. 8.4e-118;
Matches 231; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 60
DB 23 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 82
QY 61 TNLTLHYWYKNSDNDKVKQKSHYLFSEITSGCQLOKKEIHLVQYTFVVLQDPREPRQA 120
DB 83 TNLTLHYWYKNSDNDKVKQKSHYLFSEITSGCQLOKKEIHLVQYTFVVLQDPREPRQA 142
QY 121 TOMLKLQNLVTPWAPENLTLLKLSQLELANNRFLNHCLEHLVQYRTDWDHSHWTEQSV 180
DB 143 TOMLKLQNLVTPWAPENLTLLKLSQLELANNRFLNHCLEHLVQYRTDWDHSHWTEQSV 202
QY 181 DYRHKFSLPVSDGQKRYTFRVRSRNPFCGSAQHSWSHPHIGWSNTSKN 232
DB 203 DYRHKFSLPVSDGQKRYTFRVRSRNPFCGSAQHSWSHPHIGWSNTSKN 254

RESULT 10
US-08-052-205-11
Sequence 11, Application US/08052205
Patent No. 5510259
GENERAL INFORMATION:
APPLICANT: SUGAMURA, KAZUO
APPLICANT: TAKEISHITA, TOSHIKAZU

APPLICANT: SUGAMURA, KAZUO
APPLICANT: TAKEISHITA, TOSHIKAZU
APPLICANT: ASAO, HIRONOBU
APPLICANT: NAKAMURA, MASATAKA
APPLICANT: SHIMAMURA, TOSHIRO
APPLICANT: SUZUKI, MANABU
APPLICANT: HAMURO, JUNJI
TITLE OF INVENTION: HUMAN IL-2 RECEPTOR GAMMA CHAIN MOLECULE
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/052,205
FILING DATE: 19930422
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 104947/1992
FILING DATE: 23-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5510259man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-615-0X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 230 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-052-205-11

Query Match 99.1%; Score 1277; DB 1; Length 230;
Best Local Similarity 100.0%; Pred. No. 9.2e-118;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 60
DB 1 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 60
QY 61 TNLTLHYWYKNSDNDKVKQKSHYLFSEITSGCQLOKKEIHLVQYTFVVLQDPREPRQA 120
DB 61 TNLTLHYWYKNSDNDKVKQKSHYLFSEITSGCQLOKKEIHLVQYTFVVLQDPREPRQA 120
QY 121 TOMLKLQNLVTPWAPENLTLLKLSQLELANNRFLNHCLEHLVQYRTDWDHSHWTEQSV 180
DB 121 TOMLKLQNLVTPWAPENLTLLKLSQLELANNRFLNHCLEHLVQYRTDWDHSHWTEQSV 180
QY 181 DYRHKFSLPVSDGQKRYTFRVRSRNPFCGSAQHSWSHPHIGWSNTSK 230
DB 181 DYRHKFSLPVSDGQKRYTFRVRSRNPFCGSAQHSWSHPHIGWSNTSK 230

RESULT 11
US-08-595-974-11
Sequence 11, Application US/08595974
Patent No. 5705608
GENERAL INFORMATION:
APPLICANT: SUGAMURA, KAZUO
APPLICANT: TAKEISHITA, TOSHIKAZU

APPLICANT: ASAO, HIRONOBU
APPLICANT: NAKAMURA, MASATAKA
APPLICANT: SHIMAMURA, TOSHIRO
APPLICANT: SUZUKI, MANABU
APPLICANT: HAMURO, JUNJI
TITLE OF INVENTION: HUMAN IL-2 RECEPTOR GAMMA CHAIN MOLECULE
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/595,974
FILING DATE: 06-FEB-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/052,205
FILING DATE: 22-APR-1993
APPLICATION NUMBER: JP 104947/1992
FILING DATE: 23-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 570560man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-615-0X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 230 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-595-974-11

Query Match 99.1%; Score 1277; DB 1; Length 230;
Best Local Similarity 100.0%; Pred. No. 9.2e-118; Mismatches 0; Indels 0; Gaps 0;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNTLTTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 60
Db 1 LNTLTTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 60
QY 61 TNLTLHWYKNSDNDKVKQKSHYLPSEETSGCQKKEIHLVQTFVVLQDPREPRQA 120
Db 61 TNLTLHWYKNSDNDKVKQKSHYLPSEETSGCQKKEIHLVQTFVVLQDPREPRQA 120
QY 121 TQMLKQLNVLIPWAPENLTLHLKLSQLELNWNNRFLNHLVQYRTDWDHWSWTEQSV 180
Db 121 TQMLKQLNVLIPWAPENLTLHLKLSQLELNWNNRFLNHLVQYRTDWDHWSWTEQSV 180
QY 181 DYRHKESLPVDCQKRYTFRVRSRFPNPLCGSAQHSEWSHPHWSNTSK 230
Db 181 DYRHKESLPVDCQKRYTFRVRSRFPNPLCGSAQHSEWSHPHWSNTSK 230

RESULT 12
US-08-052-205-9
; Sequence 9, Application US/08052205
; Patent No. 5510259
; GENERAL INFORMATION:
; APPLICANT: SUGAMURA, KAZUO
; APPLICANT: TAKESHITA, TOSHIKAZU

APPLICANT: ASAO, HIRONOBU
APPLICANT: NAKAMURA, MASATAKA
APPLICANT: SHIMAMURA, TOSHIRO
APPLICANT: SUZUKI, MANABU
APPLICANT: HAMURO, JUNJI
TITLE OF INVENTION: HUMAN IL-2 RECEPTOR GAMMA CHAIN MOLECULE
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/052,205
FILING DATE: 19930422
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 104947/1992
FILING DATE: 23-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 551025man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-615-0X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-052-205-9

Query Match 99.1%; Score 1277; DB 1; Length 252;
Best Local Similarity 100.0%; Pred. No. 1e-117;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNTLTTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 60
Db 23 LNTLTTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 82
QY 61 TNLTLHWYKNSDNDKVKQKSHYLPSEETSGCQKKEIHLVQTFVVLQDPREPRQA 120
Db 83 TNLTLHWYKNSDNDKVKQKSHYLPSEETSGCQKKEIHLVQTFVVLQDPREPRQA 142
QY 121 TQMLKQLNVLIPWAPENLTLHLKLSQLELNWNNRFLNHLVQYRTDWDHWSWTEQSV 180
Db 143 TQMLKQLNVLIPWAPENLTLHLKLSQLELNWNNRFLNHLVQYRTDWDHWSWTEQSV 202
QY 181 DYRHKESLPVDCQKRYTFRVRSRFPNPLCGSAQHSEWSHPHWSNTSK 230
Db 203 DYRHKESLPVDCQKRYTFRVRSRFPNPLCGSAQHSEWSHPHWSNTSK 252

RESULT 13
US-08-595-974-9
; Sequence 9, Application US/08595974
; Patent No. 5705608
; GENERAL INFORMATION:
; APPLICANT: SUGAMURA, KAZUO
; APPLICANT: TAKESHITA, TOSHIKAZU
; APPLICANT: ASAO, HIRONOBU
; APPLICANT: NAKAMURA, MASATAKA

APPLICANT: SHIMAMURA, TOSHIRO
APPLICANT: SUZUKI, MANABU
APPLICANT: HAMURO, JUNJI
TITLE OF INVENTION: HUMAN IL-2 RECEPTOR GAMMA CHAIN MOLECULE
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C. Jefferson Davis Highway, Suite 400
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/595,974
FILING DATE: 06-FEB-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/052,205
FILING DATE: 22-APR-1993
APPLICATION NUMBER: JP 104947/1992
FILING DATE: 23-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5705608man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-615-0X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-595-974-9

Query Match 99.1%; Score 1277; DB 1; Length 252;
Best Local Similarity 100.0%; Pred. No. 1e-117;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTTILTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFFVNFVYMNCTWNSSEPOQ 60
DB 23 LNTTILTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFFVNFVYMNCTWNSSEPOQ 82
QY 61 TNLTLHYWYKNSDNDKVKQCSHYLFSSEITSGCOLQKKEIHLVYQTFVVLQDPREPRQA 120
DB 83 TNLTLHYWYKNSDNDKVKQCSHYLFSSEITSGCOLQKKEIHLVYQTFVVLQDPREPRQA 142
QY 121 TOMLKLQNLVLPWAPENLTHLKSQLELNWNNRFLNHCLHLVQVTRTDWDSWTSQSV 180
DB 143 TOMLKLQNLVLPWAPENLTHLKSQLELNWNNRFLNHCLHLVQVTRTDWDSWTSQSV 202
QY 181 DYRHKFLSPVSDGQKRYTFRVRSRFPNPLCGSAQHSWSESHPIHWSNTSK 230
DB 203 DYRHKFLSPVSDGQKRYTFRVRSRFPNPLCGSAQHSWSESHPIHWSNTSK 252

RESULT 14
US-08-424-224-2
; Sequence 2, Application US/08424224
; Patent No. 5912173
; GENERAL INFORMATION:
; APPLICANT: LEONARD, WARREN J.
; TITLE OF INVENTION: MURINE IL-2R CDNA AND
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVE.
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT # 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,224
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/121,435
FILING DATE: 14-SEPT-1993
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-4061US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 369
TYPE: AMINO ACID
TOPOLOGY: UNKNOWN
MOLECULE TYPE:
DESCRIPTION: PROTEIN
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: MURINE
INDIVIDUAL ISOLATE: IL-2R
US-08-424-224-2

Query Match 66.3%; Score 853.5; DB 2; Length 369;
Best Local Similarity 67.2%; Pred. No. 8e-76;
Matches 156; Conservative 33; Mismatches 42; Indels 1; Gaps 1;

QY 2 NNTTILTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFFVNFVYMNCTWNSSEPOQ 61
DB 24 SSKVILMSANEDIKADLILTSTAPEHLSAPTLPPEVQCFFVNFVYMNCTWNSSEPOQ 83
QY 62 NLTLYWYKNSDNDKVKQCSHYLFSSEITSGCOLQKKEIHLVYQTFVVLQDPREPRQA 121
DB 84 NLTLYWYKNSDNDKVKQCSHYLFSSEITSGCOLQKKEIHLVYQTFVVLQDPREPRQA 143
QY 122 QMLKLQNLVLPWAPENLTHLKSQLELNWNNRFLNHCLHLVQVTRTDWDSWTSQSV 180
DB 144 QMLKLQNLVLPWAPENLTHLKSQLELNWNNRFLNHCLHLVQVTRTDWDSWTSQSV 203
QY 181 DYRHKFLSPVSDGQKRYTFRVRSRFPNPLCGSAQHSWSESHPIHWSNTSKEN 232
DB 204 NHEPFLSPVSDGQKRYTFRVRSRFPNPLCGSAQHSWSESHPIHWSNTSKEN 255

RESULT 15
PCT-US94-02891-69
; Sequence 69, Application PC/TUS9402891
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; APPLICANT: REPRESENTED BY THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN
; APPLICANT: SERVICES
; APPLICANT: OFFICE OF TECHNOLOGY TRANSFER, NATIONAL
; APPLICANT: INSTITUTES OF HEALTH, BOX OTT, BETHESDA, MARYLAND 20892 USA
; TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: XSCID
; NUMBER OF SEQUENCES: 69

Search completed: March 3, 2004, 12:39:55
Job time : 17.3007 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 3, 2004, 12:25:04 ; Search time 8.71896 Seconds
(without alignments)
1385.519 Million cell updates/sec

Title: US-09-825-561A-4

Perfect score: 1288

Sequence: 1 LNTLTLPNGNEDTTADFFL.....QHWSEWSPTHWGSNTSKEN 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1288	100.0	369	1 CYRG HUMAN	P31785 homo sapien
2	1097	85.2	373	1 CYRG CANFA	P40321 canis famil
3	990.5	76.9	379	1 CYRG BOVIN	Q95118 bos taurus
4	853.5	66.3	369	1 CYRG MOUSE	P34902 mus musculu
5	207	16.1	380	1 IL132 HUMAN	Q14627 homo sapien
6	181.5	14.1	424	1 IL131 MOUSE	O09030 mus musculu
7	178	13.8	427	1 IL131 HUMAN	P78552 homo sapien
8	159.5	12.4	371	1 CEL2 HUMAN	Q9hc73 homo sapien
9	159	12.3	897	1 CYRB HUMAN	P32927 homo sapien
10	150	11.6	831	1 PRLR CHICK	Q04594 gallus gall
11	146.5	11.4	400	1 GPCR HUMAN	P15509 homo sapien
12	145.5	11.3	831	1 PRLR MELGA	Q31094 meleagris g
13	132.5	10.3	830	1 PRLR COLLI	Q30374 columba liv
14	132	10.2	810	1 IL4B MOUSE	P16382 mus musculu
15	125	9.7	896	1 CYRB MOUSE	P26955 mus musculu
16	121.5	9.4	581	1 PRLR BOVIN	Q28172 bos taurus
17	120	9.3	538	1 IL21R HUMAN	Q9hbe5 homo sapien
18	118	9.2	415	1 IL5R MOUSE	P21183 mus musculu
19	117.5	9.1	359	1 IL2B MOUSE	Q8ci19 mus musculu
20	116	9.0	878	1 IL13B MOUSE	P26954 mus musculu
21	114	8.9	360	1 CEL2 RAT	Q8r488 rattus norv
22	114	8.9	460	1 IL6A MOUSE	P22272 mus musculu
23	113	8.8	581	1 PRLR CEREL	Q28235 cervus elap
24	112	8.7	420	1 IL5R HUMAN	Q01344 homo sapien
25	112	8.7	918	1 IL6B HUMAN	P40189 homo sapien
26	110.5	8.6	551	1 IL2B HUMAN	P14784 homo sapien
27	109.5	8.5	608	1 PRLR MOUSE	Q08501 mus musculu
28	109	8.5	462	1 IL6A RAT	P22273 rattus norv
29	108.5	8.4	610	1 PRLR RAT	P05710 rattus norv
30	106	8.2	581	1 PRLR SHEEP	O46561 ovis aries
31	105	8.2	539	1 IL2B MOUSE	P16297 mus musculu
32	105	8.2	1356	1 CA21 ONCMY	Q93484 oncorhynchu
33	104.5	8.1	917	1 IL6B MOUSE	Q00560 mus musculu

34	104	8.1	1493	1 NEO1 MOUSE	P97798 mus musculu
35	102	7.9	611	1 GHR COLLI	Q30375 columba liv
36	100	7.8	529	1 IL21R MOUSE	Q9jhx3 mus musculu
37	98.5	7.6	918	1 IL6B RAT	P40190 rattus norv
38	97.5	7.6	467	1 IL6A PIG	O18796 sus scrofa
39	97.5	7.6	608	1 GHR CHICK	Q02092 gallus gall
40	97.5	7.6	825	1 IL4R HUMAN	P24394 homo sapien
41	96.5	7.5	625	1 TPOR MOUSE	Q08351 mus musculu
42	95.5	7.4	622	1 PRLR HUMAN	P16471 homo sapien
43	95.5	7.4	630	1 PRLR ORENI	Q91513 oreochromis
44	95.5	7.4	1461	1 NEO1 HUMAN	Q28859 homo sapien
45	95	7.4	312	1 F3ST FLABI	P52835 flaveria bi

ALIGNMENTS

RESULT 1

ID	CYRG HUMAN	STANDARD;	PRT;	369 AA.
DT	01-JUL-1993 (Rel. 26, Created)			
DT	01-JUL-1993 (Rel. 26, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Cytokine receptor common gamma chain precursor (Gamma-C) (Interleukin-2 receptor gamma chain) (IL-2R gamma chain) (P64) (CD132 antigen).			
GN	IL2RG.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]_TaxID=9606;			
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RX	MEDLINE=92335883; PubMed=1631559;			
RA	Takeshita T., Asao H., Ohtani K., Ishii N., Kumaki S., Tanaka N.,			
RA	Munakata H., Nakamura M., Sugamura K.;			
RT	"Cloning of the gamma chain of the human IL-2 receptor.";			
RL	Science 257:379-382(1992).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RX	MEDLINE=92393887; PubMed=8514792;			
RA	Noguchi M., Adelstein S., Cao X., Leonard W.J.;			
RT	"Characterization of the human interleukin-2 receptor gamma chain gene.";			
RL	J. Biol. Chem. 268:13601-13608(1993).			
RN	[3]			
RP	SEQUENCE FROM N.A., AND VARIANTS XSCID ASP-114 AND ASN-153.			
RX	MEDLINE=94004847; PubMed=8401490;			
RA	Fuck J.M., Deschenes S.M., Porter J.C., Dutra A.S., Brown C.J.,			
RA	Willard H., Henthorn P.S.;			
RT	"The interleukin-2 receptor gamma chain maps to Xq13.1 and is mutated in X-linked severe combined immunodeficiency, SCIDX1.";			
RL	Hum. Mol. Genet. 2:1099-1104(1993).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=B-cell;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.H.,			
RA	Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Munz D.W., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,			
RA	Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [5]
 RN IDENTIFICATION AS A IL-4R SUBUNIT.
 RX MEDLINE=94090315; PubMed=8266076;
 RA Kondo M., Takeshita T., Ishii N., Nakamura M., Watanabe S.,
 RA Arai K.-I., Sugamura K.;
 RT "Sharing of the interleukin-2 (IL-2) receptor gamma chain between
 RT receptors for IL-2 and IL-4";
 RL Science 262:1874-1877 (1993).
 RN [6]
 RN IDENTIFICATION AS A IL-4R SUBUNIT.
 RX MEDLINE=94090317; PubMed=8266078;
 RA Russell S.M., Kegan A.D., Harada N., Nakamura Y., Noguchi M.,
 RA Leland P., Friedmann M.C., Miyajima A., Puri R.K., Paul W.E.,
 RA Leonard W.J.;
 RT "Interleukin-2 receptor gamma chain: a functional component of the
 RT interleukin-4 receptor";
 RL Science 262:1880-1883 (1993).
 RN [7]
 RN IDENTIFICATION AS A IL-7R SUBUNIT.
 RX MEDLINE=94090316; PubMed=8266077;
 RA Noguchi M., Nakamura Y., Russell S.M., Ziegler S.F., Tsang M., Cao X.,
 RA Leonard W.J.;
 RT "Interleukin-2 receptor gamma chain: a functional component of the
 RT interleukin-7 receptor";
 RL Science 262:1877-1880 (1993).
 RN [8]
 RN 3D-STRUCTURE MODELLING OF 57-248;
 RX MEDLINE=95111955; PubMed=7529123;
 RA Bamorough P., Hedgecock C.J., Richards W.G.;
 RT "The interleukin-2 and interleukin-4 receptors studied by molecular
 RT modelling";
 RL Structure 2:839-851 (1994).
 RN [9]
 RN VARIANTS XSCID PHE-115; CYS-240 AND ILE-241.
 RX MEDLINE=94330970; PubMed=8299698;
 RA Disanto J.P., Dautry-Varsat A., Certain S., Fischer A.,
 RA de Saint Basile G.;
 RT "Interleukin-2 (IL-2) receptor gamma chain mutations in X-linked
 RT severe combined immunodeficiency disease result in the loss of
 RT high-affinity IL-2 receptor binding";
 RL Eur. J. Immunol. 24:475-479 (1994).
 RN [10]
 RN VARIANT XSCID LYS-68.
 RX MEDLINE=94375038; PubMed=8088810;
 RA Markiewicz S., Subtil A., Dautry-Varsat A., Fischer A.,
 RA de Saint Basile G.;
 RT "Detection of three nonsense mutations and one missense mutation in
 RT the interleukin-2 receptor gamma chain gene in SCIDX1 that
 RT differently affect the mRNA processing";
 RL Genomics 21:291-293 (1994).
 RN [11]
 RN VARIANT XSCID HIS-162.
 RX MEDLINE=94300093; PubMed=8027558;
 RA Ishii N., Asao H., Kimura Y., Takeshita T., Nakamura M., Tsuchiya S.,
 RA Konno T., Maeda M., Uchiyama T., Sugamura K.;
 RT "Impairment of ligand binding and growth signaling of mutant IL-2
 RT receptor gamma-chains in patients with X-linked severe combined
 RT immunodeficiency";
 RL J. Immunol. 153:1310-1317 (1994).
 RN [12]
 RN VARIANT XSCID ASN-39.
 RX MEDLINE=95023932; PubMed=7937790;
 RA Disanto J.P., Rieux-Laucat F., Dautry-Varsat A., Fischer A.,
 RA de Saint Basile G.;
 RT "Defective human interleukin 2 receptor gamma chain in an atypical X
 RT chromosome-linked severe combined immunodeficiency with peripheral T
 RT cells";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:9466-9470 (1994).
 RN [13]
 RN VARIANTS XSCID CYS-226 AND HIS-226.
 RX MEDLINE=95397841; PubMed=7668284;
 RA Pepper A.E., Buckley R.H., Small T.N., Puck J.M.;
 RT "Two mutational hotspots in the interleukin-2 receptor gamma chain
 RT gene causing human X-linked severe combined immunodeficiency";
 RL Am. J. Hum. Genet. 57:564-571 (1995).
 RN [14]
 RN VARIANT XSCID SER-183.
 RX MEDLINE=96013903; PubMed=7857965;
 RA Clark P.A., Lester T., Genet S., Jones A.M., Hendriks R.,
 RA Lavinsky R.L., Kinnon C.;
 RT "Screening for mutations causing X-linked severe combined
 RT immunodeficiency in the IL-2R gamma chain gene by single-strand
 RT conformation polymorphism analysis";
 RL Hum. Genet. 96:427-432 (1995).
 RN [15]
 RN VARIANT XSCID GLN-HIS-TRP-237 INS.
 RX MEDLINE=95164726; PubMed=7860773;
 RA Puck J.M., Pepper A.E., Bedard P.-M., Laframboise R.;
 RT "Female germ line mosaicism as the origin of a unique IL-2 receptor
 RT gamma-chain mutation causing X-linked severe combined
 RT immunodeficiency";
 RL J. Clin. Invest. 95:895-899 (1995).
 RN [16]
 RN VARIANT XSCID GLN-293.
 RX MEDLINE=95190013; PubMed=7893965;
 RA Schmaisteg F.C., Leonard W.J., Noguchi M., Berg M., Rudloff H.E.,
 RA Denney R.M., Dave S.K., Brooks E.G., Goldman A.S.;
 RT "Missense mutation in exon 7 of the common gamma chain gene causes a
 RT moderate form of X-linked combined immunodeficiency";
 RL J. Clin. Invest. 95:1169-1173 (1995).
 RN [17]
 RN VARIANT XSCID ARG-115.
 RX MEDLINE=97042245; PubMed=8900089;
 RA Stephan V., Wahn V., Le Deist F., Dirksen U., Broeker B.,
 RA Mueller-Fleckenstein I., Horneff G., Schroten H., Fischer A.,
 RA de Saint Basile G.;
 RT "Atypical X-linked severe combined immunodeficiency due to possible
 RT spontaneous reversion of the genetic defect in T cells";
 RL New Engl. J. Med. 335:1563-1567 (1996).
 RN [18]
 RN VARIANT XSCID GLN-285.
 RX MEDLINE=97295088; PubMed=9150740;
 RA Jones A.M., Clark P.A., Katz F., Genet S., McMahon C., Alterman L.,
 RA Cant A., Kinnon C.;
 RT "B-cell-negative severe combined immunodeficiency associated with a
 RT common gamma chain mutation";
 RL Hum. Genet. 99:677-680 (1997).
 RN [19]
 RN VARIANT XSCID CYS-222.
 RX MEDLINE=98064061; PubMed=9399950;
 RA Sharfe N., Shahar M., Roifman C.M.;
 RT "An interleukin-2 receptor gamma chain mutation with normal thymus
 RT morphology";
 RL J. Clin. Invest. 100:3036-3043 (1997).
 RN [20]
 RN FUNCTION: Common subunit for the receptors for a variety of
 CC interleukins.
 CC -1- SUBUNIT: The gamma chain is common to the IL2, IL4, IL7, IL21 and
 CC probably also the IL13 receptors.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- DISEASE: Defects in IL2RG are the cause of X-linked severe
 CC combined immunodeficiency (XSCID) [MIM:300400]; also known as
 CC agammaglobulinemia, Swiss type.
 CC -1- SIMILARITY: Belongs to the type I cytokine family of receptors.
 CC Subfamily 5.
 CC -1- SIMILARITY: Contains 1 fibronectin type III domain.
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD132 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd132.htm".
 CC -1- DATABASE: NAME=IL2RGbase; NOTE=X-linked SCID mutation database;
 CC WWW="http://www.hgri.nih.gov/DIR/GMB/SCID/".
 CC -----
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Query Match 100.0%; Score 1288; DB 1; Length 369;
 Best Local Similarity 100.0%; Pred. No. 3.9e-99;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTLTLPNGNEDTADPFLTTMPTDLSVSTPLPVEQCFVFNVEYMNCTWNSSEPPQ 60
 DB 23 LNTLTLPNGNEDTADPFLTTMPTDLSVSTPLPVEQCFVFNVEYMNCTWNSSEPPQ 82

QY 61 TNLTHWYKNSDNDKVKQSHYLFSEITSGCQLOKKEIHLVQTFVVLQDPRPRQA 120
 DB 83 TNLTHWYKNSDNDKVKQSHYLFSEITSGCQLOKKEIHLVQTFVVLQDPRPRQA 142

QY 121 TQMLKQLNVLVPAPENLTLLKSESQLELNWNRFLNHCLHLEHLVQRTDWDHSHWTEQSV 180
 DB 143 TQMLKQLNVLVPAPENLTLLKSESQLELNWNRFLNHCLHLEHLVQRTDWDHSHWTEQSV 202

QY 181 DYRKHPSLPSVDGQKRYTFRVRSRFPNPLCGSAQHSWSESHPIHWGNTSKEN 232
 DB 203 DYRKHPSLPSVDGQKRYTFRVRSRFPNPLCGSAQHSWSESHPIHWGNTSKEN 254

RESULT 2

CVRG CANFA STANDARD; PRT; 373 AA.

ID CVRG CANFA STANDARD; PRT; 373 AA.

AC P40321, 1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Cytokine receptor common gamma chain precursor (Gamma-C)

DE (Interleukin-2 receptor gamma chain) (IL-2R gamma chain) (P64).

EN IL2RG.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OC NCBI_TaxID=9615;

OC [1]

OC SEQUENCE FROM N.A.

OC TISSUE=Spleen;

OC MEDLINE=95130114; PubMed=7829104;

OC Henthorn P.S.; Somberg R.L.; Fimiani V.M.; Puck J.M.; Patterson D.F.,

OC Felsburg P.J.;

OC "IL-2R gamma gene microdeletion demonstrates that canine X-linked

OC severe combined immunodeficiency is a homologue of the human

OC disease.";

OC Genomics 23:69-74(1994).

OC -!- FUNCTION: Common subunit for the receptors for a variety of

OC interleukins.

OC -!- SUBUNIT: The gamma chain is common to the IL2, IL4, IL7, IL21 and

OC probably also the IL13 receptors.

OC -!- SUBCELLULAR LOCATION: Type I membrane protein.

OC -!- DISEASE: Defects in IL2RG are the cause of a canine X-linked

OC severe combined immunodeficiency.

OC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.

OC Subfamily 5.

OC -!- SIMILARITY: Contains 1 fibronectin type III domain.

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OC or send an email to license@isb-sib.ch).

OC -----

OC EMBL; U04361; AAC48403.1; --

OC PIR; A55718; A55718.

OC HSP; P31785; 11LM.

OC InterPro; IPR002996; CR1A.

OC InterPro; IPR008957; FN III-like.

OC InterPro; IPR003961; FN III.

OC InterPro; IPR003531; Hemtopoptn_S_F1.

OC SMART; SM00060; FN3; 1.

DR PROSITE; P501355; HEMATOPO REC S_F1; 1.
 KW Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 373
 FT CYTOKINE RECEPTOR COMMON GAMMA CHAIN.
 FT DOMAIN 23 261
 FT TRANSMEM 262 283
 FT DOMAIN 284 373
 FT DOMAIN 151 249
 FT DISULFID 62 72
 FT DISULFID 102 115
 FT CARBOHYD 24 24
 FT CARBOHYD 71 71
 FT CARBOHYD 75 75
 FT CARBOHYD 84 84
 FT CARBOHYD 159 159
 FT CARBOHYD 164 164
 FT CARBOHYD 249 249
 SQ SEQUENCE 373 AA; 42516 MW; 03A0DE1F8B089DBB CRC64;

Query Match 85.2%; Score 1097; DB 1; Length 373;
 Best Local Similarity 82.8%; Pred. No. 2.3e-83;
 Matches 192; Conservative 24; Mismatches 16; Indels 0; Gaps 0;

QY 1 LNTLTLPNGNEDTADPFLTTMPTDLSVSTPLPVEQCFVFNVEYMNCTWNSSEPPQ 60
 DB 23 LNSTVPMNGNEDITPDFFLTATPSETLSVSSLPPEVQCFVFNVEYMNCTWNSSEPPQ 82

QY 61 TNLTHWYKNSDNDKVKQSHYLFSEITSGCQLOKKEIHLVQTFVVLQDPRPRQA 120
 DB 83 TNLTHWYKNSDNDKVKQSHYLFSEITSGCQLOKKEIHLVQTFVVLQDPRPRQA 142

QY 121 TQMLKQLNVLVPAPENLTLLKSESQLELNWNRFLNHCLHLEHLVQRTDWDHSHWTEQSV 180
 DB 143 TQMLKQLNVLVPAPENLTLLKSESQLELNWNRFLNHCLHLEHLVQRTDWDHSHWTEQSV 202

QY 181 DYRKHPSLPSVDGQKRYTFRVRSRFPNPLCGSAQHSWSESHPIHWGNTSKEN 232
 DB 203 DYRKHPSLPSVDGQKRYTFRVRSRFPNPLCGSAQHSWSESHPIHWGNTSKEN 254

RESULT 3

CVRG BOVIN STANDARD; PRT; 379 AA.

ID CVRG BOVIN STANDARD; PRT; 379 AA.

AC Q95118;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Cytokine receptor common gamma chain precursor (Gamma-C)

DE (Interleukin-2 receptor gamma chain) (IL-2R gamma chain) (P64).

GN IL2RG.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OC NCBI_TaxID=9913;

OC [1]

OC SEQUENCE FROM N.A.

OC MEDLINE=96268473; PubMed=8672241;

OC Yoo J.; Stone R.T.; Solinas-Toldo S.; Fries R.; Beattie C.W.;

OC "Cloning and chromosomal mapping of bovine interleukin-2 receptor

OC gamma gene.";

OC DNA Cell Biol. 15:453-459(1996).

OC -!- FUNCTION: Common subunit for the receptors for a variety of

OC interleukins.

OC -!- SUBUNIT: The gamma chain is common to the IL2, IL4, IL7, IL21 and

OC probably also the IL13 receptors.

OC -!- SUBCELLULAR LOCATION: Type I membrane protein.

OC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.

OC Subfamily 5.

OC -!- SIMILARITY: Contains 1 fibronectin type III domain.

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OC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>

OC or send an email to license@isb-sib.ch).

OC -----

OC EMBL; U04361; AAC48403.1; --

OC PIR; A55718; A55718.

OC HSP; P31785; 11LM.

OC InterPro; IPR002996; CR1A.

OC InterPro; IPR008957; FN III-like.

OC InterPro; IPR003961; FN III.

OC InterPro; IPR003531; Hemtopoptn_S_F1.

OC SMART; SM00060; FN3; 1.

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EMBL; U33748; AB07812.1; -
HSSP; F31785; IILM.
InterPro; IPR002996; CRIA.
InterPro; IPR008957; FN.III-like.
InterPro; IPR003961; FN.III.
InterPro; IPR003531; Hemtopoptn_s_F1.
Pfam; PF00041; fn3; 1.
SMART; SM00060; FN3; 1.
PROSITE; PS01355; HENATOPO_REC_S_F1; 1.
Receptor; Transmembrane; Glycoprotein; signal.
KW SIGNAL 1 22
FT CHAIN 23 379
FT DOMAIN 23 269
FT TRANSMEM 270 280
FT DOMAIN 291 379
FT DOMAIN 158 256
FT DISULFID 68 78
FT DISULFID 109 122
FT CARBOHYD 77 77
FT CARBOHYD 81 81
FT CARBOHYD 90 90
FT CARBOHYD 166 166
FT CARBOHYD 171 171
SEQUENCE 379 AA; 43037 MW; 33CFAD9C9B032178 CRC64;

Query Match 76.9%; Score 990.5; DB 1; Length 379;
Best Local Similarity 76.2%; Pred. No. 1.4e-74;
Matches 182; Conservative 21; Mismatches 29; Indels 7; Gaps 2;
QY 1 LNTTILTPNGED-----TTADFLLTTPMTDSVSLPLPEVQCFFVNFVYNCNTWNS 54
DB 23 LNPFLTPSGNEDIGKPGTGDFLTTPAATDLVSTLPLPKVCFVNFVYNCNTWNS 82
QY 55 SSEPQNTLTHYWKYK-SNDKVKCKSHYLFSEBITSGCQKKEIHLVYQTFVVLQDP 113
DB 83 SSEPQNTLTHYGRNFGDDKLCQCHYLFSEGITSGCWFGRKEIRLYETFFVVLQDP 142
QY 114 RPRQATQMLKQNLVWPAPENLTNKLSEQLNWNRFNLNCHLHVQVTRTDWH 173
DB 143 REHRQPKQMLKQDLVWPAPENLTNLSFQELSNRYLDHCLHVLVQVRSRDR 202
QY 174 SWTEQSDVVRHFKFSLPSVDGQKRYFRVRSRNPFLCGSAQHSWSPHIGNSNTSKEN 232
DB 203 SWTEQSDVHRHFSFLPSVDQAQKLYFRVRSRNPFLCGSAQHSWSPHIGNSNTSKEN 261

RESULT 4
CYRG MOUSE STANDARD; PRT; 369 AA.
AC P34502;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cytokine receptor common gamma chain precursor (Gamma-C)
DE (Interleukin-2 receptor gamma chain) (IL-2R gamma chain) (P64).
GN IL2RG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCB_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=9327575; PubMed=8503926;
RX Kumaki S., Kondo M., Takeshita T., Asao H., Nakamura M., Sugamura K.;
RT "Cloning of the mouse interleukin 2 receptor gamma chain:
RT demonstration of functional differences between the mouse and human
RT receptors.";

Biochem. Biophys. Res. Commun. 193:356-363 (1993).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=CBA/CA;
RX MEDLINE=93391374; PubMed=8378320;
RA Cao X., Korak C.A., Liu Y.J., Noguchi M., O'Connell E., Leonard W.J.;
RT "Characterization of cDNAs encoding the murine interleukin 2 receptor
RT (IL-2R) gamma chain: chromosomal mapping and tissue specificity of
RT IL-2R gamma chain expression.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:8464-8468 (1993).
[3]
RN SEQUENCE FROM N.A.
RX MEDLINE=93366191; PubMed=8359699;
RA Kobayashi N., Nakagawa S., Minami Y., Taniguchi T., Kono T.;
RT "Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor
RT gamma.";
RL Gene 130:303-304 (1993).
[4]
RN SEQUENCE FROM N.A.
RX MEDLINE=95104285; PubMed=7805729;
RA Disanto J.P., Certain S., Wilson A., Macdonald H.R., Avner P.,
RA Fischer A., de Saint Basile G.;
RT "The murine interleukin-2 receptor gamma chain gene: organization,
RT chromosomal localization and expression in the adult thymus.";
RL Eur. J. Immunol. 24:3014-3018 (1994).
[5]
RN SEQUENCE FROM N.A.
RP STRAIN=B6 S;
RX MEDLINE=96341745; PubMed=8750189;
RA Chiu R.K., Droll A., Cooper D.L., Dougherty S.T., Dirks J.F.,
RA Dougherty G.J.;
RT "Molecular mechanisms regulating the hyaluronan binding activity of
RT the adhesion protein CD44.";
RL J. Neurooncol. 26:231-239 (1995).
[6]
RN SEQUENCE FROM N.A.
RP STRAIN=FVB/N; TISSUE=Salivary gland;
RX MEDLINE=922388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
RA Scapleton M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshyuki S., Carninci P., Frange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy P.H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whitting J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -1- FUNCTION: Common subunit for the receptors for a variety of
CC interleukins.
CC -1- SUBUNIT: The gamma chain is common to the IL2, IL4, IL7, IL21 and
CC probably also the IL13 receptors.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC -1- SUBFAMILY: 5.
CC -1- SIMILARITY: Contains 1 fibronectin type III domain.

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CC CC
CC EMBL; D13821; BAB02974.1; -
CC DR EMBL; U21795; AAB64279.1; -
CC DR EMBL; D13865; AAB02760.1; -
CC DR EMBL; L20048; AAB39286.1; -
CC DR EMBL; S75852; AAB32804.1; -
CC DR EMBL; S75844; AAB32904.1; JOINED.
CC DR EMBL; S75845; AAB32904.1; JOINED.
CC DR EMBL; S75847; AAB32904.1; JOINED.
CC DR EMBL; S75848; AAB32904.1; JOINED.
CC DR EMBL; S75849; AAB32904.1; JOINED.
CC DR EMBL; S75850; AAB32904.1; JOINED.
CC DR EMBL; S75851; AAB32904.1; JOINED.
CC DR EMBL; X75337; CAA53085.1; -
CC DR EMBL; BC014720; AAB14720.1; -
CC DR PIR; I49280; I49280.
CC DR HSP; P31785; I11M.
CC DR MGD; MGI:96551; l12r9.
CC DR InterPro; IPR002996; CRIA.
CC DR InterPro; IPR008957; FN III-like.
CC DR InterPro; IPR003961; FN III.
CC DR InterPro; IPR003531; Hemtopoptn_s_F1.
CC DR Pfam; PF00041; fn3; 1
CC DR SMART; SM00060; FN3; 1
CC DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; signal.
FT SIGNAL 1 22 BY SIMILARITY.
FT CHAIN 23 369 CYTOKINE RECEPTOR COMMON GAMMA CHAIN.
FT DOMAIN 23 263 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 264 284 POTENTIAL.
FT DOMAIN 285 369 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 151 250 FIBRONECTIN TYPE-III.
FT DISULFID 62 72 POTENTIAL.
FT DISULFID 102 115 POTENTIAL.
FT CARBOHYD 71 71 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 75 75 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 96 96 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 164 164 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 369 AA; 42241 MW; CB2DSAB459077AC7 CRC64;

Query Match 66.3%; Score 853.5; DB 1; Length 369;
Best Local Similarity 67.2%; Pred. No. 2.7e-63;
Matches 156; Conservative 33; Mismatches 42; Indels 1; Gaps 1;

2Y 2 NTTLTPNGEDTTADFLTTMTDLSVSTPLPLPEVQCFVFNVEYMNCTWNSSEFPQPT 61
Db 24 SSKVLMSSANEDIKADLITLSTAPEHLISAPTLPLPEVQCFVFNVEYMNCTWNSSEFPQAT 83
2Y 62 NLTHLYKNSDNDKVKCSHYLSEITSGCQOKKEIHLQYTFVVOLODPREPROAT 121
Db 84 NLTHLYRYKSDNNTFQCSHYLSEITSGCQOKEDIQYTFVVOLODPQKORRAV 143
2Y 122 QMLKLQNLVLPWAPENITLHKLSELSQLELWNNRFL-NHCLHLVQYRTDWDHSWTQSV 180
Db 144 QKLNQNLVLPWAPENITLHKLSELSQLELWNNRFL-NHCLHLVQYRTDWDHSWTQSV 203
2Y 181 DYRHKFLSPVDGKRYTFVRSPNPLCSAQHWSWPIHNGSNTSKEN 232
Db 204 NHEPRFLSPVDGKRYTFVRSPNPLCSAQHWSWPIHNGSNTSKEN 255

RESULT 5
ID I132 HUMAN STANDARD; PRT; 380 AA.
AC Q14627; C00667;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
DE Interleukin-13 receptor alpha-2 chain precursor (Interleukin-13
binding protein).

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GN IL13RA2 OR IL13R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Renal cell carcinoma;
RX MEDLINE=96279273; PubMed=8663118;
RA Caput D.; Laurent P.; Kaghad M.; Lelias J.M.; Lefort S.; Vita N.;
RA Ferrara P.;
RT "Cloning and characterization of a specific interleukin (IL)-13
RT binding protein structurally related to the IL-5 receptor alpha
RT chain.";
RL J. Biol. Chem. 271:16921-16926(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Donaldson D.D.; Whitters M.J.; Fitz L.; Neben T.; Finnerty H.;
RA Henderson S.L.; O'Hara R.M. Jr.; Turner K.J.; Wood C.R.; Collins M.;
RA Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97321053; PubMed=9177784;
RA Guo J.; Apicou F.; Mellerin M.P.; Lebeau B.; Jacques Y.; Minvielle S.;
RA "Chromosome mapping and expression of the human interleukin-13
RA receptor.";
RL Genomics 42:141-145(1997).
RN [4]
RP SEQUENCE FROM N.A.
RA Whitehead S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung, and Prostate;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg K.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;
RA Klausner R.D.; Collins F.S.; Wagner L.; Shenmen C.M.; Schuler G.D.;
RA Altschul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Bhat N.K.;
RA Hopkins R.P.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh F.;
RA Diatchenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.;
RA Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;
RA Brownstein M.J.; Usdin T.B.; Toshiyuki S.; Carninci P.; Prange C.;
RA Raha S.S.; Loughran J.A.; Peters G.J.; Abramson R.D.; Mullen J.J.;
RA Bosak S.A.; McGowan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;
RA Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;
RA Villalón D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;
RA Fahey J.; Helton E.; Kettman M.; Madan A.; Rodriguez S.; Sanchez A.;
RA Whiting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.;
RA Blakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;
RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.N.;
RA Butterfield Y.S.N.; Krzywinski M.I.; Skalska U.; Smal M.A.;
RA Schnerch A.; Schein J.E.; Jones S.J.M.; Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Binds as a monomer with high affinity to interleukin 13
CC (IL13), but not to IL4.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC -!- SIMILARITY: Subfamily 5.
CC -!- SIMILARITY: Contains 1 fibronectin type III domain.
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CC or send an email to license@isb-sib.ch)
CC -----
CC EMBL; X95302; CAA64617.1; -

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DR EMBL; U70981; AAB17170.1; -.
DR EMBL; Y08768; CAA70021.1; -.
DR EMBL; AL121878; CAD18962.1; -.
DR EMBL; BC020739; AAH20739.1; -.
DR EMBL; BC033705; AAH33705.1; -.
DR MIM; 300130; -.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005625; C:soluble fraction; TAS.
DR GO; GO:0004907; F:interleukin receptor activity; TAS.
DR GO; GO:0004871; F:signal transducer activity; TAS.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003532; Hemopoetn_S_F2.
DR Pfam; PF00441; fn3; 1.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
DR Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 26
FT CHAIN 27 380
FT DOMAIN 27 343
FT TRANSMEM 344 363
FT DOMAIN 364 380
FT DISULFID 145 155
FT CARBOHYD 115 115
FT CARBOHYD 215 215
FT CARBOHYD 290 290
FT CARBOHYD 299 299
FT SEQUENCE 380 AA; 44176 MW; 36ACB1B5562C687 CRC64;
Query Match 16.1%; Score 207; DB 1; Length 380;
Best Local Similarity 25.4%; Pred. No. 6.1e-10;
Matches 60; Conservative 46; Mismatches 106; Indels 24; Gaps 9;
QY 9 NGNEDTADFLLTWTPTDLSLSTPLPQVCFVFNVEYVNCVWSSSEPOQ-----T 61
DB 115 NGSE-VQSSAETTYWISPGIPETKVQDCVYVNWQYLLCSW-----RKGIVLDT 167
QY 62 NLTLYWYNSNDKVKSHYLFSEITSGQLQKKEIHLVYTFVQLQDPRE--PRQ 119
DB 168 NYNLFYWYEGLDH--ALQCDVYIKADQNGICRFPYLEASDYKDFVCVSSSENKPIRS 225
QY 120 ATOMKLVNLPWAPENITLKLSSQLELWNN--NRFNLHCHLEHLVQVETDWDHSWT 176
DB 226 SYTFQLQNVKPLPPVYVYTFTRSSCEIKLWSPILGPDPARCFDYELRDK--DTLLV 284
QY 177 EQSDVYRHKFLPSVDGQKRYTPFRVSRFNPLCGSAQHWSESHPIHW--GSNTSKE 231
DB 285 TATVE-NEITYTLKTTNETQLCFVVSQKNIYVSDGDIWSEWSDKQWEGEDLSKK 339
RESULT 6
ID 1131 MOUSE STANDARD; PRT; 424 AA.
AC 009030;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
DE Interleukin-13 receptor alpha-1 chain precursor (IL-13R-alpha-1) (IL-13RA-1) (Interleukin-13 binding protein) (NR4).
GN IL13RA1 OR IL13RA OR IL13R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=96133964; PubMed=8552669;
RX Hilton D.J., Zhang J.-G., Metcalf D., Alexander W.S., Nicola N.A.,
RA Willson T.A.;
RT "Cloning and characterization of a binding subunit of the interleukin 13 receptor that is also a component of the interleukin 4 receptor.";

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RL Proc. Natl. Acad. Sci. U.S.A. 93:497-501 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Brain, and Colon;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Datschenko L., Marusina A., Farmer A.A., Rubin G.M., Hong L.,
RA Sapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
FT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -1- FUNCTION: Binds IL13 with a low affinity. Together with IL4R-alpha
CC can form a functional receptor for IL13. Also serves as an
CC alternate accessory protein to the common cytokine receptor gamma
CC chain for IL4 signaling, but cannot replace the function of gamma
CC C in allowing enhanced IL2 binding activity (By similarity).
CC -1- SUBUNIT: Interleukin 13 receptor is a complex of IL4R, IL13RA1,
CC and possibly other components (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Spleen, liver, thymus, heart, lung, kidney,
CC testis, stomach, brain, skin, and colon; but not skeletal muscle.
CC -1- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC Subfamily 5.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; S80963; AAB50695.1; -.
DR EMBL; BC052425; AAH52425.2; -.
DR EMBL; BC059939; AAH59939.1; -.
DR MGD; MGI:105052; Il13ral.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003532; Hemopoetn_S_F2.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
DR Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 25
FT CHAIN 26 424
FT DOMAIN 26 340
FT TRANSMEM 341 364
FT DOMAIN 365 424
FT DISULFID 44 93
FT DISULFID 132 142
FT DISULFID 171 183
FT CARBOHYD 35 35
FT CARBOHYD 59 59
FT CARBOHYD 103 103
FT CARBOHYD 136 136
FT CARBOHYD 262 262
FT CARBOHYD 338 338
FT SEQUENCE 424 AA; 48402 MW; EB8330A0DC82C9F9 CRC64;

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Query Match 14.1%; Score 181.5; DB 1; Length 424;
Best Local Similarity 27.6%; Pred. No. 8.8e-08;
Matches 56; Conservative 38; Mismatches 86; Indels 23; Gaps 9;
QY 37 EVQCFFVNEVMCTWSSSPQ-P-TNLTLYWYKNSDNDKVKCSH-YLPSSEITSGCQ 94
Db 129 ELKCIWNLNWKCSWLPGRNTSDPTHTLYWY--SSLEKSCQENIYREGQHIACSPK 186
QY 95 LQKKEIHL-YQTFVVLQDPREPRQATQMLKQNLVWPAPENLTLLKLSQLELNWN 153
Db 187 LTKVEPSFPHQVIMVKNAGKIRPSKIVSLTSYVKP-DPHIKHLLKNGALLVQWK 245
QY 154 N--RELNHCLEHLVQY---RFD-----WDHSWTEQSDVDYRHKFLPSVDGQKRY 197
Db 246 NPQFRGRCLTYEVVNTQDRNILEVEDKQNSDRNMEGTSCFQLPGLVADAVY 305
QY 198 TFRVRSRFLPC-GSAQHWSEWS 219
Db 306 TVRVKTNKLCFDDNKLWSDWS 328
RESULT 7
ID 1131 HUMAN STANDARD; PRT; 427 AA.
AC P78552; Q95646; Q99656;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Interleukin-13 receptor alpha-1 chain precursor (IL-13R-alpha-1) (IL-
13RA-1) (CD213a1 antigen).
DE 1131RA1 OR IL13RA OR IL13R.
DS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC NCBI_TaxID=9606;
CC [1]
SEQUENCE FROM N.A.
RC TISSUE=Carcinoma;
RX MEDLINE=97165986; PubMed=9013879;
RA Miloux B., Laurent P., Bonnin O., Lupker J., Caput D., Vita N.,
RA Ferrara P.;
RA "Cloning of the human IL-13R alpha chain and reconstitution with the
RA IL4R alpha of a functional IL-4/IL-13 receptor complex.";
RA FEBS Lett. 401:163-166 (1997).
[2]
SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RA Gauchat J.F.M., Schlagenhauf E., Feng N.P., Moser R., Yamage M.,
RA Jeannin P., Alouani S., Elson G., Notarangelo L.D., Wells T.,
RA Eugster H.P., Bonnesfey J.Y.;
RA Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RX MEDLINE=97067184; PubMed=8910586;
RA Anan M.J., Tayebi N., Obiri N.I., Puri R.K., Modi W.S.,
RA Leonard W.J.;
RA "cDNA cloning and characterization of the human interleukin 13
RA receptor alpha chain.";
RA J. Biol. Chem. 271:29265-29270 (1996).
[4]
SEQUENCE FROM N.A.
RA Wada M., Hisano T., Kuwano M.;
RA Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
[5]
SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX MEDLINE=22398257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Ussdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquelland N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherth A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- FUNCTION: Binds IL13 with a low affinity. Together with IL4R-alpha
CC can form a functional receptor for IL13. Also serves as an
CC alternate accessory protein to the common cytokine receptor gamma
CC chain for IL4 signaling, but cannot replace the function of gamma
CC C in allowing enhanced IL2 binding activity.
CC -!- SUBUNIT: Interleukin 13 receptor is a complex of IL4R, IL13RA1,
CC and possibly other components.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Ubiquitous. Highest levels in heart, liver,
CC skeletal muscle and ovary; lowest levels in brain, lung and
CC kidney. Also found in B-cells, T-cells and endothelial cells.
CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC Subfamily 5.
CC -!- DATABASE: NAME=PROW; NOTE=PROW 2:95-100(2001);
CC WWW="http://www.ncbi.nlm.nih.gov/prow/guide/435859885.g.htm".

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CC EMBL; Y10659; CAA71669.1; -;
CC EMBL; Y09328; CAA70508.1; -;
CC EMBL; U62858; AAB37127.1; -;
CC EMBL; U81379; AAD00510.3; -;
CC EMBL; BC009960; AAO09960.1; -;
CC Genew; HGNC:5974; IL13RA1.
CC MIM; 300119; -;
CC GO; GO:0005898; C:interleukin-13 receptor complex; TAS.
CC GO; GO:0005886; C:plasma membrane; TAS.
CC GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
CC InterPro; IPR002996; CR1A.
CC InterPro; IPR008957; FN III-like.
CC PROSITE; PS01356; HEMATOPOIETIN F2.
CC Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 21
FT CHAIN 22 427 INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN.
FT DOMAIN 22 343 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 344 367 POTENTIAL.
FT DOMAIN 368 427 CYTOPLASMIC (POTENTIAL).
FT DISULFID 46 95 POTENTIAL.
FT DISULFID 134 144 BY SIMILARITY.
FT DISULFID 173 185 BY SIMILARITY.
FT CARBOHYD 37 37 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 61 61 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 105 105 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 138 138 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 235 235 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 265 265 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 329 329 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 341 341 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 130 130 T -> I (IN REF. 3).

FT VARIANT 652 652 V -> M (in dBSNP:1801114).
FT /FTID=VAR.014803.
SQ SEQUENCE 897 AA; 97335 MW; 3398B37FDB8F393A CRC64;

Query Match 12.3%; Score 159; DB 1; Length 897;
Best Local Similarity 26.4%; Pred. No. 1.6e-05;
Matches 55; Conservative 40; Mismatches 79; Indels 34; Gaps 12;

QY 38 VQCFVFNVEYMNCTWNSSE-PQPTNLTLYHYKNSDNDKVKQCS-...HYLFSEETSGC 93
DB 248 LECFPDGAVALSCSEWEVRKE-VASSVSFGLFYKSPDAGEBECSPVLREGLSLHTRHC 306

QY 94 QLOKKEIHLTYQTFVVOLODPREPQATQMLKONLVIWPAPENLTLHKLSESOLELWN 153
DB 307 QIPVDPDPATHQGIIVSVQ-...PRR-AEKHLK-SVNIQWAPPELNTKQDGS-YSLRWE 359

QY 154 NRLFNLHCLHEH-...VQYRTD-...WDHSMTEQSVYRHKFSLPSVDGQKRYTFRVRSR- 204
DB 360 TMKREY--EHIDHTFEIQYKRDATKQDSKTE-TLQNAHSMALPALSPTRYWARVVRT 416

QY 205 ----FNPLCGSAQHSEWSHPHWSNT 228
DB 417 SRTGYNGI-----WSEWSEARSMDTES 438

RESULT 10
PRLR CHICK
ID PRLR CHICK STANDARD; PRT; 831 AA.
AC Q04594;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Prolactin receptor precursor (PRL-R) (CPRLP).
GN PRLR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White leghorn; TISSUE=Kidney;
RX MEDLINE=93075121; PubMed=1445292;
RA Tanaka M., Maeda K., Okubo T., Nakashima K.;
RT "Double antenna structure of chicken prolactin receptor deduced from the cDNA sequence."
RL Biochem. Biophys. Res. Commun. 188:490-496(1992).
CC -!- FUNCTION: This is a receptor for the anterior pituitary hormone prolactin.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors. Subfamily 1.
CC -!- SIMILARITY: Contains 4 fibronectin type III domains.
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CC -----
CC EMBL; D13154; BAA02439.1; --
CC PIR; JQ1655; JQ1655.
CC HSSP; P16471; IEP3.
CC InterPro; IPR002996; CRIA.
CC InterPro; IPR008957; FN III-like.
CC InterPro; IPR003961; FN III.
CC InterPro; IPR003528; Hemopoetn_L_F1.
CC Pfam; PF00041; fn3. 4.
CC SMART; SM00060; FN3. 3.
CC PROSITE; PS01352; HEMATOPO REC_L_F1; 1.
CC Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
KW

FT SIGNAL 1 23
FT CHAIN 24 831
FT DOMAIN 24 831
FT TRANSMEM 439 459
FT CYTOPLASMIC (POTENTIAL).
FT FIBRONECTIN TYPE-III 1.
FT FIBRONECTIN TYPE-III 2.
FT FIBRONECTIN TYPE-III 3.
FT FIBRONECTIN TYPE-III 4.
FT BY SIMILARITY.
FT DISULFID 36 46
FT DISULFID 75 86
FT CARBOHYD 59 59
FT CARBOHYD 91 91
FT CARBOHYD 100 100
FT CARBOHYD 112 112
FT CARBOHYD 122 122
FT CARBOHYD 262 262
FT CARBOHYD 303 303
FT CARBOHYD 315 315
FT CARBOHYD 335 335
SQ SEQUENCE 831 AA; 94102 MW; 104E75791DCADBE9 CRC64;

Query Match 11.6%; Score 150; DB 1; Length 831;
Best Local Similarity 25.0%; Pred. No. 7.9e-05;
Matches 50; Conservative 34; Mismatches 90; Indels 26; Gaps 9;

QY 38 VQCFVFNVEYMNCTWNSSE-PQPTNLTLYHYKNSDNDKVKQSHYLFSEETSG-...C 93
DB 34 ICRSLEKETPSCWMPGSDGLPTNYTL--FYSKDSEIEVECPDYR-...-TSGPNSC 86

QY 94 QLOKKEIHLTYQTFVVOLODPREPQAT--QMLKONLVIWPAPENLTLHKLSESOLEL 150
DB 87 YFNKHTSPWTTFTTATNTEIGNSSDPQVDVTSIVQGPSVNLTLTKRSANIMYL 146

QY 151 --NWNRF-...-NHCLHLVQYRTDWDHSMTEQSVYRHKFSLPSVDGQKRYTFRVRS 203
DB 147 WAKWSPPLADASSNHLHYELRIKPEEKEWETISVGVTQCKINRLNAGRYVYVQVRC 206

QY 204 RFNPLCGSAQHSEWSHPH 223
DB 207 TLDP-----GEWSEWSERH 221

RESULT 11
GMCR HUMAN
ID GMCR HUMAN STANDARD; PRT; 400 AA.
AC P15509; Q00207; Q14429; Q14430; Q14431; Q16564;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Granulocyte-macrophage colony-stimulating factor receptor alpha chain precursor (GM-CSF-R-alpha) (GMR) (CDw116) (CD116 antigen).
GN (CSF2RA OR CSF2RA OR CSF2R OR CSF2RX) AND (CSF2RAY OR CSF2RA OR CSF2R OR CSF2RY).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Placenta;
RX MEDLINE=90059966; PubMed=2555171;
RA Gearing D.P., King J.A., Gough N.M., Nicola N.A.;
RT "Expression cloning of a receptor for human granulocyte-macrophage colony-stimulating factor."
RL EMBL J. 8:3667-3676(1989).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=94193800; PubMed=8144676;
RA Nakagawa Y., Kosegi H., Miyajima A., Arai K.-I., Yokota T.;
RT "Structure of the gene encoding the alpha subunit of the human granulocyte-macrophage colony stimulating factor receptor.
RT Implications for the evolution of the cytokine receptor

Db 185 VQTOCKINRLNAGMYVYVQVRCMLDP-----GKSEWS 217

RESULT 13

PRLR COLLI STANDARD; PRT; 830 AA.
AC Q90374;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Prolactin receptor precursor (PRL-R).
GN PRLR.
OS Columba livia (Domestic pigeon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Columbiformes; Columbidae; Columba.
OX NCBI_TaxID=8932;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=CropSac;
RX MEDLINE=94283267; PubMed=7516866;
RA Chen X., Horseman N.D.;
RT "Cloning, expression, and mutational analysis of the pigeon prolactin receptor.";
RL Endocrinology 135:269-276(1994).
CC -!- FUNCTION: This is a receptor for the anterior pituitary hormone prolactin.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors. Subfamily 1.
CC -!- SIMILARITY: Contains 4 fibronectin type III domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC
CC EMBL; U07694; AAA20646.1; -
CC F1R; I50455; I50455.
CC HSP; P16471; I1B3.
CC InterPro; IPR002996; CRLA.
CC InterPro; IPR008957; FN III-like.
CC InterPro; IPR003961; FN III.
CC InterPro; IPR003528; Hemtopoptn_L_F1.
CC Pfam; PF00041; fn3; 4.
CC SMART; SM00060; FN3; 4.
CC PROSITE; PS01352; HEMATOPO RECL_F1; 1.
CC Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 23
FT CHAIN 24 830 PROLACTIN RECEPTOR.
FT DOMAIN 24 439 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 440 460 POTENTIAL.
FT DOMAIN 461 830 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25 122 FIBRONECTIN TYPE-III 1.
FT DOMAIN 123 226 FIBRONECTIN TYPE-III 2.
FT DOMAIN 229 326 FIBRONECTIN TYPE-III 3.
FT DOMAIN 327 429 FIBRONECTIN TYPE-III 4.
FT DISULFID 36 46 BY SIMILARITY.
FT DISULFID 75 86 BY SIMILARITY.
FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 304 304 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 316 316 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 830 AA; 94507 MW; 3B074E83CDF69E9F CRC64;

Query Match

10.3%; Score 132.5; DB 1; Length 830;

Best Local Similarity 22.2%; Pred. No. 0.0022;
Matches 44; Conservative 37; Mismatches 96; Indels 21; Gaps 7;
QY 38 VOCFVFNVEYMNCTWNSSE-PQPTNLTLYWYKNSDNDKVKQKSHYLFSEBITSGCQLQ 96
DB 34 IRCRSLEKETFCWKPKGSDGGLPTNYTL--FYKSDSEKIYECPDYMGSG--PNSCYFD 89
QY 97 KKEIHLHYQTFVYVQLQDPREPRQAT--QWLKLNLYIWPAPENLTILH---KLSESOLEIN 151
DB 90 KHNTPWTITNITVYMAINEIGNSSDPQVVDVTISVQDPAPVNLSTETKTASTITLLAK 149
QY 152 WNNRFL-----NHCLHLVQYRTDHSWTSQSDYVYRHKFSLPSVDGQKRYTFVRSRF 205
DB 150 WSPPLADVTNSHVYRYELRLKPEKEWETVSGVQTYKVNRLQAGVYVQVRCVL 209
QY 206 NPLCGSAQHWSEWSPHPIH 223
DB 210 D-----IGWSEWSSSRH 222

RESULT 14

IL4R MOUSE
ID IL4R MOUSE STANDARD; PRT; 810 AA.
AC P16382;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Interleukin-4 receptor alpha chain precursor (IL-4R-alpha).
GN IL4R OR IL4RA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.; SEQUENCE OF 26-39; 162-179 AND 194-210, AND ALTERNATIVE SPLICING
RX MEDLINE=90030408; PubMed=2805066;
RA Mosley B., Beckmann M.P., March C.J., Idzerda R.L., Gimpel S.D., Vanden Bos T., Friend D., Albert A., Anderson D., Jackson J., Wignall J.M., Smith C., Gallis B., Sims J.E., Urdal D., Widmer M.B., Cosman D., Park L.S.;
RA "The murine interleukin-4 receptor: molecular cloning and characterization of secreted and membrane bound forms.";
RT Cell 59:335-348(1989).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=90138976; PubMed=2405398;
RA Harada N., Castle B.E., Gorman D.M., Itoh N., Schreurs J., Barrett R.L., Howard M., Miyajima A.;
RA "Expression cloning of a cDNA encoding the murine interleukin 4 receptor based on ligand binding.";
RT Proc. Natl. Acad. Sci. U.S.A. 87:857-861(1990).
RL -!- FUNCTION: This is a receptor for interleukin-4. The soluble form of the IL4 receptor may represent a regulatory molecule specific for IL4-dependent immune responses.
CC -!- SUBUNIT: Heterodimer of an alpha chain and a common gamma chain.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein and secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=3;
CC Name=1; Synonyms=Membrane;
CC IsoId=P16382-1; Sequence=Displayed;
CC Note=Binds IL-4;
CC Name=2; Synonyms=Secreted;
CC IsoId=P16382-2; Sequence=VSP_001675, VSP_001676;
CC Note=Binds IL-4;
CC Name=3;
CC IsoId=P16382-3; Sequence=VSP_001677;
CC Note=Lacks the cytoplasmic domain. Binds IL-4;
CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors. Subfamily 4.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation -

Db 412 YCARVRVK--PISNYDGIWSKWSSEYTW 437

Search completed: March 3, 2004, 12:36:12
Job time : 9.71896 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 3, 2004, 12:38:15 ; Search time 30.3268 Seconds
(without alignments)
1615.322 Million cell updates/sec

Title: US-09-825-561A-4

Perfect score: 1288

Sequence: 1 LNTTILPNGNEDTTADFFL.....QHWSEWHPHGSNTSKEN 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	1288	100.0	232	9	US-09-825-561A-4
2	1288	100.0	360	9	US-09-825-561A-18
3	1288	100.0	369	15	US-10-116-275-339
4	1288	100.0	691	9	US-09-935-868-20
5	1288	100.0	691	14	US-10-287-035-20
6	1288	100.0	691	14	US-10-282-162-20
7	1288	100.0	694	9	US-09-935-868-18
8	1288	100.0	694	9	US-09-935-868-22
9	1288	100.0	694	14	US-10-287-035-18
10	1288	100.0	694	14	US-10-287-035-22
11	1288	100.0	694	14	US-10-282-162-18
12	1288	100.0	694	14	US-10-282-162-22
13	1282	99.5	482	9	US-09-824-286-2
14	990.5	76.9	379	13	US-10-078-059-3
15	960	74.5	363	10	US-09-376-430-3

16	853.5	66.3	369	9	US-09-895-943-12	Sequence 12, Appl
17	853.5	66.3	369	9	US-09-895-593-12	Sequence 12, Appl
18	215	16.7	561	9	US-09-828-995B-72	Sequence 72, Appl
19	215	16.7	561	9	US-09-828-995B-81	Sequence 81, Appl
20	215	16.7	563	9	US-09-828-995B-78	Sequence 78, Appl
21	215	16.7	565	9	US-09-828-995B-75	Sequence 75, Appl
22	213	16.5	318	9	US-09-828-995B-69	Sequence 69, Appl
23	213	16.5	365	9	US-09-828-995B-66	Sequence 66, Appl
24	213	16.5	386	9	US-09-828-995B-61	Sequence 61, Appl
25	207	16.1	317	9	US-09-825-561A-84	Sequence 84, Appl
26	207	16.1	380	8	US-08-815-773-2	Sequence 2, Appl
27	207	16.1	380	9	US-09-871-617-2	Sequence 2, Appl
28	207	16.1	380	9	US-09-780-926-1	Sequence 1, Appl
29	207	16.1	380	10	US-09-090-867-2	Sequence 2, Appl
30	207	16.1	380	13	US-10-104-408-1	Sequence 1, Appl
31	206	16.0	255	9	US-09-828-995B-58	Sequence 58, Appl
32	203	15.8	380	8	US-08-815-773-4	Sequence 4, Appl
33	203	15.8	380	10	US-09-090-867-4	Sequence 4, Appl
34	183.5	14.2	372	8	US-08-815-773-7	Sequence 7, Appl
35	183.5	14.2	372	10	US-09-090-867-7	Sequence 7, Appl
36	181	14.1	776	14	US-10-287-035-36	Sequence 36, Appl
37	181	14.1	776	14	US-10-287-035-40	Sequence 40, Appl
38	181	14.1	776	14	US-10-287-035-44	Sequence 44, Appl
39	180	14.0	426	13	US-10-036-568-2	Sequence 2, Appl
40	179	13.9	778	9	US-09-935-868-46	Sequence 46, Appl
41	179	13.9	778	9	US-09-935-868-50	Sequence 50, Appl
42	179	13.9	778	14	US-10-287-035-46	Sequence 46, Appl
43	179	13.9	778	14	US-10-287-035-50	Sequence 50, Appl
44	179	13.9	778	14	US-10-287-035-56	Sequence 56, Appl
45	179	13.9	778	14	US-10-287-035-60	Sequence 60, Appl

ALIGNMENTS

RESULT 1

US-09-825-561A-4
; Sequence 4, Application US/09825561A
; Patent No. US2002013767A1
; GENERAL INFORMATION:
; APPLICANT: No. US2002013767A1ak, Julia E.
; APPLICANT: West, James W., Scott R.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHALL CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; PRIOR FILING DATE: 2000-04-05
; PRIOR FILING DATE: 2000-04-05
; PRIOR FILING DATE: 2000-04-05
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-561A-4

Query Match 100.0%; Score 1288; DB:9; Length 232;
Best Local Similarity 100.0%; Pred. No. 1.3e+118; Indels 0; Gaps 0;
Matches 232; Conservative 0; Mismatches 0;
QY 1 LNTTILPNGNEDTTADFFLTTMTDLSVSTPLPEVQCFVFNVEYMNCTWNSSEPPQ 60
Db 1 LNTTILPNGNEDTTADFFLTTMTDLSVSTPLPEVQCFVFNVEYMNCTWNSSEPPQ 60
QY 61 TNLTHWYKNSNDKVKCKSHYLFSEETSGCLOKKEHLYCTFVQLODPRPRQA 120
Db 61 TNLTHWYKNSNDKVKCKSHYLFSEETSGCLOKKEHLYCTFVQLODPRPRQA 120

QY 121 TQMLKQLNLVIPWAPENLTLLHKLSSQLELNNRFLNHLCHLVQVYRTDWDHWSWTEQSV 180
DB 121 TQMLKQLNLVIPWAPENLTLLHKLSSQLELNNRFLNHLCHLVQVYRTDWDHWSWTEQSV 180
QY 181 DYRHKFSPLPSVDGQKRYTFRVRSRFPNPLCGSAQHSWSHPIHWSNTSKEN 232
DB 181 DYRHKFSPLPSVDGQKRYTFRVRSRFPNPLCGSAQHSWSHPIHWSNTSKEN 232

RESULT 2

US-09-825-561A-18
; Sequence 18, Application US/09825561A
; Patent No. US20020137677A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHALL CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: soluble human IL-2Rgamma/human kappa light chain
; OTHER INFORMATION: polypeptide
US-09-825-561A-18

Query Match 100.0%; Score 1288; DB 9; Length 360;
Best Local Similarity 100.0%; Pred. No. 2.3e-118;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEFPQ 60
DB 23 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEFPQ 82
QY 61 TNLTHYWKNSDNDKVKCHYLFPSEITSGCOLQKKEIHLVQYRTDWDHWSWTEQSV 120
DB 83 TNLTHYWKNSDNDKVKCHYLFPSEITSGCOLQKKEIHLVQYRTDWDHWSWTEQSV 142
QY 121 TQMLKQLNLVIPWAPENLTLLHKLSSQLELNNRFLNHLCHLVQVYRTDWDHWSWTEQSV 180
DB 143 TQMLKQLNLVIPWAPENLTLLHKLSSQLELNNRFLNHLCHLVQVYRTDWDHWSWTEQSV 202
QY 181 DYRHKFSPLPSVDGQKRYTFRVRSRFPNPLCGSAQHSWSHPIHWSNTSKEN 232
DB 203 DYRHKFSPLPSVDGQKRYTFRVRSRFPNPLCGSAQHSWSHPIHWSNTSKEN 254

RESULT 3

US-10-116-275-339
; Sequence 339, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and

; TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
; FILE REFERENCE: E10672/20087
; CURRENT APPLICATION NUMBER: US/10/116,275
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 339
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Rat
; ORGANISM: Rat
US-10-116-275-339

Query Match 100.0%; Score 1288; DB 15; Length 369;
Best Local Similarity 100.0%; Pred. No. 2.4e-118;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEFPQ 60
DB 23 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEFPQ 82
QY 61 TNLTHYWKNSDNDKVKCHYLFPSEITSGCOLQKKEIHLVQYRTDWDHWSWTEQSV 120
DB 83 TNLTHYWKNSDNDKVKCHYLFPSEITSGCOLQKKEIHLVQYRTDWDHWSWTEQSV 142
QY 121 TQMLKQLNLVIPWAPENLTLLHKLSSQLELNNRFLNHLCHLVQVYRTDWDHWSWTEQSV 180
DB 143 TQMLKQLNLVIPWAPENLTLLHKLSSQLELNNRFLNHLCHLVQVYRTDWDHWSWTEQSV 202
QY 181 DYRHKFSPLPSVDGQKRYTFRVRSRFPNPLCGSAQHSWSHPIHWSNTSKEN 232
DB 203 DYRHKFSPLPSVDGQKRYTFRVRSRFPNPLCGSAQHSWSHPIHWSNTSKEN 254

RESULT 4

US-09-935-868-20
; Sequence 20, Application US/09935868
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 691
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-868-20

Query Match 100.0%; Score 1288; DB 9; Length 691;
Best Local Similarity 100.0%; Pred. No. 5.4e-118;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEFPQ 60
DB 23 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEFPQ 82
QY 61 TNLTHYWKNSDNDKVKCHYLFPSEITSGCOLQKKEIHLVQYRTDWDHWSWTEQSV 120
DB 83 TNLTHYWKNSDNDKVKCHYLFPSEITSGCOLQKKEIHLVQYRTDWDHWSWTEQSV 142
QY 121 TQMLKQLNLVIPWAPENLTLLHKLSSQLELNNRFLNHLCHLVQVYRTDWDHWSWTEQSV 180
DB 143 TQMLKQLNLVIPWAPENLTLLHKLSSQLELNNRFLNHLCHLVQVYRTDWDHWSWTEQSV 202
QY 181 DYRHKFSPLPSVDGQKRYTFRVRSRFPNPLCGSAQHSWSHPIHWSNTSKEN 232
DB 203 DYRHKFSPLPSVDGQKRYTFRVRSRFPNPLCGSAQHSWSHPIHWSNTSKEN 254

RESULT 5

S-10-287-035-20

Sequence 20, Application US/10287035

Publication No. US20030104567A1

GENERAL INFORMATION:

APPLICANT: Neil Stahl and George D. Yancopoulos

TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING

FILE REFERENCE: REG 203DA

CURRENT APPLICATION NUMBER: US/10/287,035

PRIOR FILING DATE: 2002-11-01

PRIOR APPLICATION NUMBER: USSN 09/935,868

PRIOR FILING DATE: 2001-08-23

PRIOR APPLICATION NUMBER: USSN 09/787,835

PRIOR FILING DATE: 2001-03-22

PRIOR APPLICATION NUMBER: USSN 09/313,942

PRIOR FILING DATE: 1999-05-19

PRIOR APPLICATION NUMBER: 09/313,942

PRIOR FILING DATE: 1999-05-19

PRIOR APPLICATION NUMBER: 60/101,858

PRIOR FILING DATE: 1998-09-25

NUMBER OF SEQ ID NOS: 60

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 20

LENGTH: 691

TYPE: PRT

ORGANISM: Homo sapiens

S-10-287-035-20

Query Match

Best Local Similarity 100.0%; Score 1288; DB 14; Length 691;

Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 LNTTLTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPOP 60

b 23 LNTTLTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPOP 82

Y 61 TNLTHWYKNSDNDKVQKSHYLFSEETSGCOLQKKEIHLVQYTFVVOLODPREPRQA 120

b 83 TNLTHWYKNSDNDKVQKSHYLFSEETSGCOLQKKEIHLVQYTFVVOLODPREPRQA 142

Y 121 TOMLKLQNLVWPAPENLTJHKLSESOLELNNRFLNHCLEHLVQYRTDWDHSWTEQSV 180

b 143 TOMLKLQNLVWPAPENLTJHKLSESOLELNNRFLNHCLEHLVQYRTDWDHSWTEQSV 202

Y 181 DYRKFSLPVSDGQKRYTFRVRSRFPNPLCGSAQHWSEWHPHWSNTSKEN 232

b 203 DYRKFSLPVSDGQKRYTFRVRSRFPNPLCGSAQHWSEWHPHWSNTSKEN 254

RESULT 6

S-10-282-162-20

Sequence 20, Application US/10282162

Publication No. US20030143697A1

GENERAL INFORMATION:

APPLICANT: REGENERON PHARMACEUTICALS, INC.

TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING

FILE REFERENCE: REG 203-B-US

CURRENT APPLICATION NUMBER: US/10/282,162

PRIOR FILING DATE: 2002-10-28

PRIOR APPLICATION NUMBER: 09/787,835

PRIOR FILING DATE: 1999-09-22

PRIOR APPLICATION NUMBER: PCT/US99/22045

PRIOR FILING DATE: 1999-09-22

NUMBER OF SEQ ID NOS: 56

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 20

LENGTH: 691

TYPE: PRT

ORGANISM: Homo sapiens

S-10-282-162-20

Query Match 100.0%; Score 1288; DB 14; Length 691;
Best Local Similarity 100.0%; Pred. No. 5.4e-118;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTTLTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPOP 60

Db 23 LNTTLTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPOP 82

QY 61 TNLTHWYKNSDNDKVQKSHYLFSEETSGCOLQKKEIHLVQYTFVVOLODPREPRQA 120

Db 83 TNLTHWYKNSDNDKVQKSHYLFSEETSGCOLQKKEIHLVQYTFVVOLODPREPRQA 142

QY 121 TOMLKLQNLVWPAPENLTJHKLSESOLELNNRFLNHCLEHLVQYRTDWDHSWTEQSV 180

Db 143 TOMLKLQNLVWPAPENLTJHKLSESOLELNNRFLNHCLEHLVQYRTDWDHSWTEQSV 202

QY 181 DYRKFSLPVSDGQKRYTFRVRSRFPNPLCGSAQHWSEWHPHWSNTSKEN 232

Db 203 DYRKFSLPVSDGQKRYTFRVRSRFPNPLCGSAQHWSEWHPHWSNTSKEN 254

RESULT 7

US-09-935-868-18

Sequence 18, Application US/09935868

Patent No. US20020164690A1

GENERAL INFORMATION:

APPLICANT: Regeneron Pharmaceuticals, Inc.

TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using

CURRENT APPLICATION NUMBER: US/09/935,868

CURRENT FILING DATE: 2002-04-11

PRIOR APPLICATION NUMBER: PCT/US99/22045

PRIOR FILING DATE: 1999-09-22

NUMBER OF SEQ ID NOS: 52

SOFTWARE: Patent in version 3.0

SEQ ID NO 18

LENGTH: 694

TYPE: PRT

ORGANISM: Homo sapiens

US-09-935-868-18

Query Match

Best Local Similarity 100.0%; Score 1288; DB 9; Length 694;

Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTTLTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPOP 60

Db 23 LNTTLTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPOP 82

QY 61 TNLTHWYKNSDNDKVQKSHYLFSEETSGCOLQKKEIHLVQYTFVVOLODPREPRQA 120

Db 83 TNLTHWYKNSDNDKVQKSHYLFSEETSGCOLQKKEIHLVQYTFVVOLODPREPRQA 142

QY 121 TOMLKLQNLVWPAPENLTJHKLSESOLELNNRFLNHCLEHLVQYRTDWDHSWTEQSV 180

Db 143 TOMLKLQNLVWPAPENLTJHKLSESOLELNNRFLNHCLEHLVQYRTDWDHSWTEQSV 202

QY 181 DYRKFSLPVSDGQKRYTFRVRSRFPNPLCGSAQHWSEWHPHWSNTSKEN 232

Db 203 DYRKFSLPVSDGQKRYTFRVRSRFPNPLCGSAQHWSEWHPHWSNTSKEN 254

RESULT 8

US-09-935-868-22

Sequence 22, Application US/09935868

Patent No. US20020164690A1

GENERAL INFORMATION:

APPLICANT: Regeneron Pharmaceuticals, Inc.

TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using

CURRENT APPLICATION NUMBER: US/09/935,868

CURRENT FILING DATE: 2002-04-11

; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-868-22

Query Match 100.0%; Score 1288; DB 9; Length 694;
Best Local Similarity 100.0%; Pred. No. 5.5e-118;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNTTLTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 60
DB 23 LNTTLTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 82
QY 61 TNLTHYWKNSDNDKVKCQSHYLFSEITSGCQLOKKEIHLIYQTFVVOLODPREPRQA 120
DB 83 TNLTHYWKNSDNDKVKCQSHYLFSEITSGCQLOKKEIHLIYQTFVVOLODPREPRQA 142
QY 121 TQMLKQLNVLIPWAPENLTLLKLSQLELNWNRFLNHCLEHLVQYRTDWDHSHWTEQSV 180
DB 143 TQMLKQLNVLIPWAPENLTLLKLSQLELNWNRFLNHCLEHLVQYRTDWDHSHWTEQSV 202
QY 181 DYRKHFSLPSVDGQKRYTFRVRSRFPNLCGSAQHWSEWSHPHIGSNTSKEN 232
DB 203 DYRKHFSLPSVDGQKRYTFRVRSRFPNLCGSAQHWSEWSHPHIGSNTSKEN 254

RESULT 9

US-10-287-035-18
; Sequence 18, Application US/10287035
; Publication No. US20030104567A1
; GENERAL INFORMATION:
; APPLICANT: Neil Stahl and George D. Yancopoulos
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203DA
; CURRENT APPLICATION NUMBER: US/10/287,035
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US99/935,868
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: US99/787,835
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US99/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match 100.0%; Score 1288; DB 14; Length 694;
Best Local Similarity 100.0%; Pred. No. 5.5e-118;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNTTLTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 60
DB 23 LNTTLTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 82
QY 61 TNLTHYWKNSDNDKVKCQSHYLFSEITSGCQLOKKEIHLIYQTFVVOLODPREPRQA 120
DB 83 TNLTHYWKNSDNDKVKCQSHYLFSEITSGCQLOKKEIHLIYQTFVVOLODPREPRQA 142
QY 121 TQMLKQLNVLIPWAPENLTLLKLSQLELNWNRFLNHCLEHLVQYRTDWDHSHWTEQSV 180
DB 143 TQMLKQLNVLIPWAPENLTLLKLSQLELNWNRFLNHCLEHLVQYRTDWDHSHWTEQSV 202
QY 181 DYRKHFSLPSVDGQKRYTFRVRSRFPNLCGSAQHWSEWSHPHIGSNTSKEN 232
DB 203 DYRKHFSLPSVDGQKRYTFRVRSRFPNLCGSAQHWSEWSHPHIGSNTSKEN 254

US-10-287-035-18

Query Match 100.0%; Score 1288; DB 14; Length 694;
Best Local Similarity 100.0%; Pred. No. 5.5e-118;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTTLTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 60
DB 23 LNTTLTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 82
QY 61 TNLTHYWKNSDNDKVKCQSHYLFSEITSGCQLOKKEIHLIYQTFVVOLODPREPRQA 120
DB 83 TNLTHYWKNSDNDKVKCQSHYLFSEITSGCQLOKKEIHLIYQTFVVOLODPREPRQA 142
QY 121 TQMLKQLNVLIPWAPENLTLLKLSQLELNWNRFLNHCLEHLVQYRTDWDHSHWTEQSV 180

DB 143 TQMLKQLNVLIPWAPENLTLLKLSQLELNWNRFLNHCLEHLVQYRTDWDHSHWTEQSV 202
QY 181 DYRKHFSLPSVDGQKRYTFRVRSRFPNLCGSAQHWSEWSHPHIGSNTSKEN 232
DB 203 DYRKHFSLPSVDGQKRYTFRVRSRFPNLCGSAQHWSEWSHPHIGSNTSKEN 254

RESULT 10

US-10-287-035-22
; Sequence 22, Application US/10287035
; Publication No. US20030104567A1
; GENERAL INFORMATION:
; APPLICANT: Neil Stahl and George D. Yancopoulos
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203DA
; CURRENT APPLICATION NUMBER: US/10/287,035
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US99/935,868
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: US99/787,835
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US99/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-287-035-22
Query Match 100.0%; Score 1288; DB 14; Length 694;
Best Local Similarity 100.0%; Pred. No. 5.5e-118;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNTTLTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 60
DB 23 LNTTLTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 82
QY 61 TNLTHYWKNSDNDKVKCQSHYLFSEITSGCQLOKKEIHLIYQTFVVOLODPREPRQA 120
DB 83 TNLTHYWKNSDNDKVKCQSHYLFSEITSGCQLOKKEIHLIYQTFVVOLODPREPRQA 142
QY 121 TQMLKQLNVLIPWAPENLTLLKLSQLELNWNRFLNHCLEHLVQYRTDWDHSHWTEQSV 180
DB 143 TQMLKQLNVLIPWAPENLTLLKLSQLELNWNRFLNHCLEHLVQYRTDWDHSHWTEQSV 202
QY 181 DYRKHFSLPSVDGQKRYTFRVRSRFPNLCGSAQHWSEWSHPHIGSNTSKEN 232
DB 203 DYRKHFSLPSVDGQKRYTFRVRSRFPNLCGSAQHWSEWSHPHIGSNTSKEN 254

US-10-287-035-22

Query Match 100.0%; Score 1288; DB 14; Length 694;
Best Local Similarity 100.0%; Pred. No. 5.5e-118;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNTTLTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 60
DB 23 LNTTLTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 82
QY 61 TNLTHYWKNSDNDKVKCQSHYLFSEITSGCQLOKKEIHLIYQTFVVOLODPREPRQA 120
DB 83 TNLTHYWKNSDNDKVKCQSHYLFSEITSGCQLOKKEIHLIYQTFVVOLODPREPRQA 142
QY 121 TQMLKQLNVLIPWAPENLTLLKLSQLELNWNRFLNHCLEHLVQYRTDWDHSHWTEQSV 180
DB 143 TQMLKQLNVLIPWAPENLTLLKLSQLELNWNRFLNHCLEHLVQYRTDWDHSHWTEQSV 202
QY 181 DYRKHFSLPSVDGQKRYTFRVRSRFPNLCGSAQHWSEWSHPHIGSNTSKEN 232
DB 203 DYRKHFSLPSVDGQKRYTFRVRSRFPNLCGSAQHWSEWSHPHIGSNTSKEN 254

RESULT 11

US-10-282-162-18
; Sequence 18, Application US/10282162
; Publication No. US20030143697A1
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22

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; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-18

Query Match      100.0%; Score 1288; DB 14; Length 694;
Best Local Similarity 100.0%; Pred. No. 5.5e-118; Indels 0; Gaps 0;
Matches 232; Conservative 0; Mismatches 0;

2y 1 LNTTILTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 60
Db 23 LNTTILTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 82

2y 61 TNLTLHYWYKNSDNDKVKCSHYLFSEITSGCOLQKKEIHLVQTFVVLQDPRPRQA 120
Db 83 TNLTLHYWYKNSDNDKVKCSHYLFSEITSGCOLQKKEIHLVQTFVVLQDPRPRQA 142

2y 121 TOMLKLQNLVTPWAPENLTLHKLSEOLELNNRFLNHCLHLEHLVQRTDWDHSHWTEQSV 180
Db 143 TOMLKLQNLVTPWAPENLTLHKLSEOLELNNRFLNHCLHLEHLVQRTDWDHSHWTEQSV 202

2y 181 DYRHKFSPLPSVDGQKRYTFRVRSRFPNPLCGSAQHSWSHPHIGWSNTSKEN 232
Db 203 DYRHKFSPLPSVDGQKRYTFRVRSRFPNPLCGSAQHSWSHPHIGWSNTSKEN 254

RESULT 12
US-10-282-162-22
; Sequence 22, Application US/10282162
; Publication No. US20030143697A1
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; PRIOR FILING DATE: 2002-10-28
; PRIOR FILING DATE: 1999-09-22
; PRIOR FILING DATE: 1999-09-22
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-22

Query Match      100.0%; Score 1288; DB 14; Length 694;
Best Local Similarity 100.0%; Pred. No. 5.5e-118; Indels 0; Gaps 0;
Matches 232; Conservative 0; Mismatches 0;

2y 1 LNTTILTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 60
Db 23 LNTTILTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 82

2y 61 TNLTLHYWYKNSDNDKVKCSHYLFSEITSGCOLQKKEIHLVQTFVVLQDPRPRQA 120
Db 83 TNLTLHYWYKNSDNDKVKCSHYLFSEITSGCOLQKKEIHLVQTFVVLQDPRPRQA 142

2y 121 TOMLKLQNLVTPWAPENLTLHKLSEOLELNNRFLNHCLHLEHLVQRTDWDHSHWTEQSV 180
Db 143 TOMLKLQNLVTPWAPENLTLHKLSEOLELNNRFLNHCLHLEHLVQRTDWDHSHWTEQSV 202

2y 181 DYRHKFSPLPSVDGQKRYTFRVRSRFPNPLCGSAQHSWSHPHIGWSNTSKEN 232
Db 203 DYRHKFSPLPSVDGQKRYTFRVRSRFPNPLCGSAQHSWSHPHIGWSNTSKEN 254
```

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RESULT 13
US-09-824-286-2
; Sequence 2, Application US/09824286
; Patent No. US20020028202A1
; GENERAL INFORMATION:
; APPLICANT: Burkly, Linda C
; Benjamin, Christopher D
; Hession, Catherine A
; Whitty, Adrian
; TITLE OF INVENTION: COMMON GAMMA CHAIN BLOCKING AGENTS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/824,286
; FILING DATE: 02-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/017,466
; FILING DATE: 10-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A006 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 679-2000
; TELEFAX: 617 679-2838
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 482 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: YES
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-824-286-2

Query Match      99.5%; Score 1282; DB 9; Length 482;
Best Local Similarity 99.6%; Pred. No. 1.3e-117; Indels 0; Gaps 0;
Matches 231; Conservative 0; Mismatches 1;

Qy 1 LNTTILTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 60
Db 23 LNTTILTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 82

Qy 61 TNLTLHYWYKNSDNDKVKCSHYLFSEITSGCOLQKKEIHLVQTFVVLQDPRPRQA 120
Db 83 TNLTLHYWYKNSDNDKVKCSHYLFSEITSGCOLQKKEIHLVQTFVVLQDPRPRQA 142

Qy 121 TOMLKLQNLVTPWAPENLTLHKLSEOLELNNRFLNHCLHLEHLVQRTDWDHSHWTEQSV 180
Db 143 TOMLKLQNLVTPWAPENLTLHKLSEOLELNNRFLNHCLHLEHLVQRTDWDHSHWTEQSV 202

Qy 181 DYRHKFSPLPSVDGQKRYTFRVRSRFPNPLCGSAQHSWSHPHIGWSNTSKEN 232
Db 203 DYRHKFSPLPSVDGQKRYTFRVRSRFPNPLCGSAQHSWSHPHIGWSNTSKEN 254

RESULT 14
US-10-078-059-3
; Sequence 3, Application US/10078059
```

Publication No. US20020193305A1

GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Cytokine Receptor Common Gamma Chain Like
FILE REFERENCE: PF456P2
CURRENT APPLICATION NUMBER: US/10/078,059
CURRENT FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: 60/269,876
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: PCT/US00/22493
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: 09/376,430
PRIOR FILING DATE: 1999-08-18
PRIOR APPLICATION NUMBER: 09/263,626
PRIOR FILING DATE: 1999-03-05
PRIOR APPLICATION NUMBER: PCT/US99/05068
PRIOR FILING DATE: 1999-03-05
PRIOR APPLICATION NUMBER: 60/086,505
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/078,563
PRIOR FILING DATE: 1998-03-19
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 379
TYPE: PRT
ORGANISM: Homo sapiens
US-10-078-059-3

Query Match 76.9%; Score 990.5; DB 13; Length 379;
Best Local Similarity 76.2%; Pred. No. 4.8e-89;
Matches 182; Conservative 21; Mismatches 29; Indels 7; Gaps 2;
QY 1 LNTTILTPNGNED-----TTADFFLTMTPTDLSVSTLPLPEVQCFFVFNVEYMNCTWNS 54
DB 23 LNPKEFTPSGNEIDGKPGCTGGDFLTSTPAGTLDVSTLPLPKVQCFFVFNVEYMNCTWNS 82
QY 55 SSEPQPTNLTHWYKN-SDNDKVKQKSHYLFSEITSGCQLOKKEIHLVYTFVVQLQDP 113
DB 83 SSEPQPTNLTHWYKNFNGDKLQECGHYLFSEITSGCWFGEIHLVYTFVVQLQDP 142
QY 114 REPRQATQMLKQLNVLVPAWENITLHKLSEQLNWNRRFLNHLVQYRTDWDH 173
DB 143 REHRQPKQMLKQLDVLVPAWENITLRLSEFQLELSNRYLDHCLVQYRSRDR 202
QY 174 SWTEQSVYRHKFSLPSVDGQKRYTFVRSRFNPCLGSAQHSWSESHPIHWSNTSKEN 232
DB 203 SWTEQSVDRHRSFSLPSVDAQKLYTFVRSRYNPLCGSAQHSWSDWSYPIHWSNTSKEN 261

RESULT 15

US-09-376-430-3
Sequence 3, Application US/09376430
Publication No. US20030028006A1
GENERAL INFORMATION:
APPLICANT: Moore, Paul A.
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Cytokine Receptor Common Gamma Chain Like
FILE REFERENCE: PF456P1
CURRENT APPLICATION NUMBER: US/09/376,430
CURRENT FILING DATE: 1999-08-19
EARLIER APPLICATION NUMBER: 60/086,505
EARLIER FILING DATE: 1998-05-22
EARLIER APPLICATION NUMBER: 60/078,563
EARLIER FILING DATE: 1998-03-19
EARLIER APPLICATION NUMBER: 09/263,626
EARLIER FILING DATE: 1999-03-05
EARLIER APPLICATION NUMBER: PCT/US99/05068
EARLIER FILING DATE: 1999-03-05
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3

LENGTH: 363
TYPE: PRT
ORGANISM: Homo sapiens
US-09-376-430-3

Query Match 74.5%; Score 960; DB 10; Length 363;
Best Local Similarity 76.0%; Pred. No. 4.6e-86;
Matches 177; Conservative 20; Mismatches 32; Indels 4; Gaps 2;
QY 1 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFFVFNVEYMNCTWNSSEPO 60
DB 16 LNEDI---GKPGCTGGDFLTSTPAGTLDVSTLPLPKVQCFFVFNVEYMNCTWNSSEPO 72
QY 61 TNLTHWYKN-SDNDKVKQKSHYLFSEITSGCQLOKKEIHLVYTFVVQLQDPREPRQ 119
DB 73 NNLTHWYKNFNGDKLQECGHYLFSEITSGCWFGEIHLVYTFVVQLQDPREHRQ 132
QY 120 ATOMLKLQNLVPAWENITLHKLSEQLNWNRRFLNHLVQYRTDWDHSWTQ 179
DB 133 PQMLKQLDVLVPAWENITLRLSEFQLELSNRYLDHCLVQYRSRDRDRSWTQ 192
QY 180 VDYRHKFSLPSVDGQKRYTFVRSRFNPCLGSAQHSWSESHPIHWSNTSKEN 232
DB 193 VDRHRSFSLPSVDAQKLYTFVRSRYNPLCGSAQHSWSDWSYPIHWSNTSKEN 245

Search completed: March 3, 2004, 12:50:51
Job time : 31.3268 secs

GenCore version 5.1.6
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3M protein - protein search, using sw model

run on: March 3, 2004, 13:31:49 ; Search time 15,5425 Seconds

(without alignments)
1435,834 Million cell updates/sec

Title: US-09-825-561A-4

Perfect score: 1288

Sequence: 1 LNTLTTPNGNEDTTADFFL.....QHWSEWSHPIHGSNTSKEN 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1288	100.0	369	2 A42565	interleukin-2 rece
2	1097	85.2	373	2 A55718	interleukin-2 rece
3	853.5	66.3	369	2 I49280	interleukin-2 rece
4	427.5	33.2	348	2 JC7907	common cytokine re
5	168.5	13.1	426	2 JC7773	IL-13Ralpha 1 prot
6	159	12.3	897	1 A39255	cytokine receptor
7	150	11.6	831	2 J01655	prolactin receptor
8	146.5	11.4	400	2 S06945	granulocyte-macrop
9	145.5	11.3	333	2 SI3884	granulocyte-macrop
10	136.5	10.6	896	2 I56563	interleukin-3 rece
11	135.5	10.5	378	2 S50040	granulocyte-macrop
12	132.5	10.3	830	2 I50455	prolactin receptor
13	132	10.2	810	1 A33380	interleukin-4 rece
14	125	9.7	896	1 A35782	cytokine receptor
15	121.5	9.4	581	2 I45971	prolactin receptor
16	119.5	9.3	800	1 S31575	interleukin-4 rece
17	118	9.2	415	2 SI2357	interleukin-5 rece
18	116	9.0	878	1 A40091	interleukin-3 rece
19	114	8.9	440	2 JLO144	interleukin-6 rece
20	114	8.9	460	2 JLO145	interleukin-6 rece
21	113	8.8	420	2 S21052	interleukin-5 rece
22	112	8.7	918	2 A36337	membrane glycoprot
23	110.5	8.6	359	2 JC7280	cytokine receptor-
24	110.5	8.6	551	2 A30342	interleukin-2 rece
25	109.5	8.5	292	2 I77525	prolactin receptor
26	109.5	8.5	303	2 I77524	prolactin receptor
27	109.5	8.5	608	2 I53269	prolactin receptor
28	108.5	8.4	310	2 A29884	prolactin receptor
29	108.5	8.4	412	2 A41070	prolactin receptor

30	108.5	8.4	610	2 A34631	lactogen receptor
31	108.5	8.4	610	2 A36116	prolactin receptor
32	107	8.3	335	2 A40267	interleukin-5 rece
33	105	8.2	539	2 A35052	interleukin-2 rece
34	104.5	8.1	286	2 S50039	granulocyte-macrop
35	104.5	8.1	917	2 I49699	glycoprotein 130 -
36	98.5	7.6	918	2 A44257	interleukin-6 sign
37	97.5	7.6	608	2 S32823	somatotropin recep
38	97.5	7.6	825	1 A50386	interleukin-4 rece
39	96.5	7.5	626	2 S35317	hematopoietic grow
40	96.5	7.5	626	2 S37622	proto-oncogene - m
41	95.5	7.4	288	2 B59405	prolactin receptor
42	95.5	7.4	376	2 A59405	prolactin receptor
43	95.5	7.4	622	2 A40144	prolactin receptor
44	95.5	7.4	630	2 I51086	prolactin receptor
45	94.5	7.3	26926	1 I38344	titin, cardiac mus

ALIGNMENTS

RESULT 1

A42565

interleukin-2 receptor gamma chain - human

C:Species: Homo sapiens (man)

C>Date: 04-Mar-1993 #sequence revision 18-Nov-1994 #text_change 17-Mar-2003

C:Accession: A42565; A46591; I54332

R:Takeishi, T.; Asao, H.; Ohtani, K.; Ishii, N.; Kumaki, S.; Tanaka, N.; Munakata, H.;

Science 257, 379-382, 1992

A>Title: Cloning of the gamma chain of the human IL-2 receptor.

A:Reference number: A42565; MUID:92335883; PMID:1631559

A:Accession: A42565

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid; protein

A:Residues: 1-369 <TAK>

A:Cross-references: NID:G303611; PIDN:BAA01857.1; PID:G219890

A:Experimental source: MOLT beta lymphoid cells

A>Note: sequence extracted from NCB1 Backbone (NCBIP:109167)

R:Noguchi, M.; Adelstein, S.; Cao, X.; Leonard, W.J.

J. Biol. Chem. 268, 13601-13608, 1993

A>Title: Characterization of the human interleukin-2 receptor gamma chain gene.

A:Reference number: A46591; MUID:93293887; PMID:8514792

A:Accession: A46591

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-369 <RES>

A:Cross-references: GB:L12183; NID:G307056; PIDN:AAA59145.1; PID:G307058

R:Puck, J.M.; Deschenes, S.M.; Porter, J.C.; Dutra, A.S.; Brown, C.J.; Willard, H.F.; He

Hum. Mol. Genet. 2, 1099-1104, 1993

A>Title: The interleukin-2 receptor gamma chain maps to Xq13.1 and is mutated in X-link

A:Reference number: I54332; MUID:94004847; PMID:8401490

A:Accession: I54332

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-369 <RES2>

A:Cross-references: GB:L19546; NID:G349631; PIDN:AAC37524.1; PID:G349632

C:Genetics:

A:Gene: GDB:IL2RG; SCIDX1: IMD4

A:Cross-references: GDB:I34807; OMIM:308380

A:Map position: Xq13.1-Xq13.1

A:Introns: 39/1; 90/2; 152/1; 198/3; 253/1; 285/2; 308/3

A>Note: defects are associated with an X-linked form of severe combined immunodeficiency

C:Superfamily: interleukin-2 receptor gamma chain

C:Keywords: cytokine receptor; duplication; immunodeficiency; transmembrane protein

Query Match 100.0%; Score 1288; DB 2; Length 369;

Best Local Similarity 100.0%; Pred. No. 7.7e+100; Indels 0; Gaps 0;

Matches 232; Conservative 0; Mismatches 0;

QY 1 LNTLTTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFFVFNVEYMNCTWNSSEPPQ 60

Db 23 LNTLTTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFFVFNVEYMNCTWNSSEPPQ 82

QY 61 TNLTLHYWYKNSDNDKVKQCSHYLSSEITSGCOLQKKEIHLVQYFVVLQDPPREPRQA 120
 Db 83 TNLTLHYWYKNSDNDKVKQCSHYLSSEITSGCOLQKKEIHLVQYFVVLQDPPREPRQA 142
 QY 121 TQMLKLQNLVLPWAPENLTLHLKLSSEQLNWNRFNLHCLSEHLVQYRTDWDHWSWTEQSV 180
 Db 143 TQMLKLQNLVLPWAPENLTLHLKLSSEQLNWNRFNLHCLSEHLVQYRTDWDHWSWTEQSV 202
 QY 181 DYRHKFSPLSDVGQKRYTFRVRSRNPPLCGSAQHSWSESHPIHWSNTSKEN 232
 Db 203 DYRHKFSPLSDVGQKRYTFRVRSRNPPLCGSAQHSWSESHPIHWSNTSKEN 254
 RESULT 2
 A55718
 Interleukin-2 receptor gamma chain precursor - dog
 C:Species: Canis lupus familiaris (dog)
 C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 23-Jul-1999
 C:Accession: A55718
 R:Henthorn, P.S.; Somborg, R.L.; Fimiani, V.M.; Puck, J.M.; Patterson, D.F.; Felsburg, F.
 Genomics 23, 69-74, 1994
 A:Title: IL-2Rgamma Gene microdeletion demonstrates that canine X-linked severe combined
 A:Reference number: A55718; MUID:95130114; PMID:7829104
 A:Accession: A55718
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-373 <GEN>
 A:Cross-references: GB:U04361; NID:9517411; PIDN:AA048403.1; PID:9517412
 C:Superfamily: Interleukin-2 receptor gamma chain
 C:Keywords: cytokine receptor, duplication
 Query Match 85.2%; Score 1097; DB 2; Length 373;
 Best Local Similarity 82.8%; Pred. No. 6.4e-84;
 Matches 192; Conservative 24; Mismatches 16; Indels 0; Gaps 0;
 QY 1 LNTTLTPNGNEDTTADPFLTTMPTDSLSVSTLPLPEVQCFVFNVEYVNCNTWNGSSSEPOP 60
 Db 23 LNSTVPMNGNEDITDPFLTATPBTETLSVSLPLPEVQCFVFNVEYVNCNTWNGSSSEPRP 82
 QY 61 TNLTLHYWYKNSDNDKVKQCSHYLSSEITSGCOLQKKEIHLVQYFVVLQDPPREPRQA 120
 Db 83 TNLTLHYWYKNSDNDKVKQCSHYLSSEITSGCOLQKKEIHLVQYFVVLQDPPREPRQA 142
 QY 121 TQMLKLQNLVLPWAPENLTLHLKLSSEQLNWNRFNLHCLSEHLVQYRTDWDHWSWTEQSV 180
 Db 143 TQMLKLQNLVLPWAPENLTLHLKLSSEQLNWNRFNLHCLSEHLVQYRTDWDHWSWTEQSV 202
 QY 181 DYRHKFSPLSDVGQKRYTFRVRSRNPPLCGSAQHSWSESHPIHWSNTSKEN 232
 Db 203 DYRHKFSPLSDVGQKRYTFRVRSRNPPLCGSAQHSWSESHPIHWSNTSKEN 254
 RESULT 3
 I49280
 Interleukin-2 receptor gamma chain precursor - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 20-Jun-2000
 C:Accession: I49280; A47514; JN0592; JN0775; S37582; I53398
 R:Cao, X.; Kozak, C.A.; Liu, Y.
 Proc. Natl. Acad. Sci. U.S.A. 90, 8464-8468, 1993
 A:Title: Characterization of cDNAs encoding the murine interleukin 2 receptor (IL-2R) ga
 A:Reference number: A47514; MUID:93391374; PMID:8378320
 A:Accession: I49280
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-369 <CAO>
 A:Cross-references: EMBL:U21795; NID:9727349; PIDN:AAA64279.1; PID:9727350
 A:Accession: A47514
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-369 <RE2>
 A:Cross-references: GB:L20048; NID:9404067; PIDN:AAA39286.1; PID:9404068
 R:Kumaki, S.; Kondo, M.; Takeshita, T.; Aeao, H.; Nakamura, M.; Sugamura, K.

Biochem. Biophys. Res. Commun. 193, 356-363, 1993
 A:Title: Cloning of the mouse interleukin 2 receptor gamma chain: Demonstration of func
 A:Reference number: JN0592; MUID:93277575; PMID:8503926
 A:Accession: JN0592
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-369 <KUM>
 A:Cross-references: DDBJ:D13565; NID:9303684; PIDN:BA02760.1; PID:9303685
 R:Kobayashi, N.; Nakagawa, S.; Minami, Y.; Taniguchi, T.; Kono, T.
 Gene 130, 303-304, 1993
 A:Title: Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor gamma.
 A:Reference number: JN0775; MUID:93366191; PMID:8359699
 A:Accession: JN0775
 A:Molecule type: mRNA
 A:Residues: 1-369 <KOB>
 A:Cross-references: GB:D13921; NID:9436045; PIDN:BA02974.1; PID:9436046
 R:Chiu, R.K.; Dougherty, G.J.
 submitted to the EMBL Data Library, October 1993
 A:Description: Regulation of CD44-mediated cellular adhesion by the IL-2 R gamma chain.
 A:Reference number: S37582
 A:Accession: S37582
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-350, 'S', 352-366, 'S', 368-369 <CHI>
 A:Cross-references: EMBL:X75337
 R:Disanto, J.P.; Certain, S.; Wilson, A.; MacDonald, H.R.; Avner, P.; Fischer, A.; de S
 Eur. J. Immunol. 24, 3014-3018, 1994
 A:Title: The murine interleukin-2 receptor gamma chain gene: organization, chromosomal
 A:Reference number: I53398; MUID:95104285; PMID:7805729
 A:Accession: I53398
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-369 <RES>
 A:Cross-references: GB:S75852; NID:9861554; PIDN:AAB32904.1; PID:9861555
 C:Genetics:
 A:Gene: IL-2Rgamma
 A:Introns: 39/1; 90/2; 152/1; 199/3; 254/1; 286/2; 308/3
 C:Complex: The high affinity receptor is a heterotrimer of alpha (see PIR:UHMS2), beta
 eptors.
 C:Function:
 A:Description: receptor for interleukin-2
 A:Pathway: interleukin-2 stimulated growth and differentiation of T cells, B cells, NK
 C:Superfamily: Interleukin-2 receptor gamma chain
 C:Keywords: cytokine receptor; duplication; glycoprotein; transmembrane protein
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-369/Product: interleukin-2 receptor gamma chain #status predicted <MAT>
 F:256-284/Domain: transmembrane #status predicted <TM>
 F:71,75,84,96,159,164,306/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 66.3%; Score 853.5; DB 2; Length 369;
 Best Local Similarity 67.2%; Pred. No. 1.2e-63;
 Matches 156; Conservative 33; Mismatches 42; Indels 1; Gaps 1;
 QY 2 NNTLTTPNGNEDTTADPFLTTMPTDSLSVSTLPLPEVQCFVFNVEYVNCNTWNGSSSEPOP 61
 Db 24 SSKVLMSANEDIKADLIITSTAPBHLAPTLPPEVQCFVFNVEYVNCNTWNGSSSEPOP 83
 QY 62 NLTLHYWYKNSDNDKVKQCSHYLSSEITSGCOLQKKEIHLVQYFVVLQDPPREPRQA 121
 Db 84 NLTLHYWYKNSDNDKVKQCSHYLSSEITSGCOLQKKEIHLVQYFVVLQDPPREPRQA 143
 QY 122 QMLKLQNLVLPWAPENLTLHLKLSSEQLNWNRFNLHCLSEHLVQYRTDWDHWSWTEQSV 180
 Db 144 QMLKLQNLVLPWAPENLTLHLKLSSEQLNWNRFNLHCLSEHLVQYRTDWDHWSWTEQSV 203
 QY 181 DYRHKFSPLSDVGQKRYTFRVRSRNPPLCGSAQHSWSESHPIHWSNTSKEN 232
 Db 204 NHEPFLSPLSDVGQKRYTFRVRSRNPPLCGSAQHSWSESHPIHWSNTSKEN 255
 RESULT 4
 JC7907
 common cytokine receptor gamma chain, isoform a - chicken

```
C:Species: Gallus gallus (chicken)
C>Date: 03-Feb-2003 #sequence_revision 03-Feb-2003 #text_change 31-Mar-2003
C:Accession: JC7907
R:Min, W.; Lillehoj, H.S.; Fetterer, R.H.
Biochem. Biophys. Res. Commun. 299, 321-327, 2002
A:Title: Identification of an alternatively spliced isoform of the common cytokine receptor
A:Reference number: JC7907; MUID:22325486; PMID:12437989
A:Accession: JC7907
A:Molecule type: mRNA
A:Residues: 1-348 <MIN>
A:Cross-references: GB:AJ419897; GB:AJ419898
A:Experimental source: egg
A:Comment: This protein, expressed as a transmembrane glycoprotein, is a novel member of
nont and proliferation.
2:Genetics:
A:Gene: ch gamma-c-a

Query Match 33.2%; Score 427.5; DB 2; Length 348;
Best Local Similarity 42.9%; Pred. No. 3.5e-28;
Matches 91; Conservative 36; Mismatches 56; Indels 29; Gaps 9;

2y 34 PLPE-VOCFVFNVEYMNCTWNSSEPOPTNLTLHYWYKNSDNDKVKCSHYLSEITSG 92
Db 24 PSPAGVSCILFNESYMTCTW-GSCQTITANYSLYIYEN--KLPVVECCQYLWDRSVRIG 80
2y 93 CQLOKKEIHLHYQTFFVQ-----LQDPRPRRQATQMLKQLNVLIPWAPENLTHLKL 143
Db 81 CRPEQSEIIQFAPYVRVNASCNQQTLEIP-----SNRMELQNLVKPEAPVNLTIHNM 133
2y 144 SESQLELWNNRF-LNKLCHLHVQYRTDWDHSWTEQSVDRHK---FSLPSVDGQKRYTF 199
Db 134 SGNOLQLTWSPSPYKPCQCLHVVVKYKSKDTSWNTQEV----KGVIFSPSPVDYERKYTF 189
2y 200 RVSRFNPPLCGSAQHWSEWGHPIHWGNS-TSK 230
Db 190 YRSKINNYCGNTQLNSENSEVPVFWGNNSTSK 221

RESULT 5
JC7773
IL-13Ralpha 1 protein - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C:Accession: JC7773
R:Pierrot, C.; Beniguel, L.; Begue, A.; Khalife, J.
Biochem. Biophys. Res. Commun. 287, 969-976, 2001
A:Title: Expression of a functional IL-13Ralpha1 by rat B cells.
A:Reference number: JC7773; PMID:11573960
A:Accession: JC7773
A:Molecule type: mRNA
A:Residues: 1-426 <PIE>
A:Cross-references: GB:AY044251
A:Comment: This protein is an functionally binding protein involved in B cell proliferation
2:Genetics:
A:Gene: il-13ralpha1

Query Match 13.1%; Score 168.5; DB 2; Length 426;
Best Local Similarity 25.5%; Pred. No. 1.7e-06;
Matches 54; Conservative 30; Mismatches 101; Indels 27; Gaps 8;

2y 37 EVQCFVFNVEYMNCTWNSSEPOPTNLTLHYWYKNSDNDKVKCSHYLSEITSGCQL 95
Db 129 ELQCTWNLNLYMKSWLPGKNTSPDNTLYIYVY--SSLGKSLQCN-THREQHIGCSF 185
2y 96 QKEI----HLVQTFVVLQDPRPRRQATQMLKQLNVLIPWAPENLTHLKLSQLELW 152
Db 186 KLTKVESNVEHNTIQLMVKNAGKIRPSYKIVSFTSNVKEGPHIHLF-LKNGALFVQW 244
2y 153 NN--RFLNHLCHLHVQYRTDWDHSWTEQSVDRHK-----FSLPSVDGQ 194
Db 245 KNQPFSSRCLSLSEVENVSTQTSYNSNSLEVEDKQNSFDPNMEGASCFISPGVLN 304
2y 195 KRYTFVRVSRFNPILC-GSAQHWSEWSPHIHWG 225

Db 305 TTYTVRVVRVTKNKLCFDDNDLWSNWSALSIG 336
|||||:|||||:|||||:
RESULT 6
A39255
cytokine receptor common beta chain precursor - human
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 27-Oct-2003
C:Accession: A39255
R:Hayashida, K.; Kitamura, T.; Gorman, D.M.; Arai, K.; Yokota, T.; Miyajima, A.
Proc. Natl. Acad. Sci. U.S.A. 87, 9655-9659, 1990
A:Title: Molecular cloning of a second subunit of the receptor for human granulocyte-macrophage colony-stimulating factor
A:Reference number: A39255; MUID:91088571; PMID:1702217
A:Accession: A39255
A:Molecule type: mRNA
A:Residues: 1-897 <HAY>
A:Cross-references: GB:M38275
A:Comment: The human high-affinity IL-3, IL-5, and GM-CSF receptors have ligand-specific
C:Genetics:
A:Gene: GDB:CSF2RB
A:Cross-references: GDB:126838; OMIM:138981
A:Map position: 22q13.1-22q13.1
C:Superfamily: Interleukin (IL)-3/IL-5/GM-CSF receptor common beta chain; cytokine recep
C:Keywords: alternative splicing; cytokine receptor; duplication; transmembrane protein
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-897/Product: cytokine receptor common beta chain #status predicted <EXT>
F:17-443/Domain: extracellular #status predicted <EXT>
F:35-232/Domain: cytokine receptor homology <CRS1>
F:250-431/Domain: cytokine receptor homology <CRS2>
F:444-460/Domain: transmembrane #status predicted <TM>
F:461-897/Domain: intracellular #status predicted <INT>

Query Match 12.3%; Score 159; DB 1; Length 897;
Best Local Similarity 26.4%; Pred. No. 2.6e-05;
Matches 55; Conservative 40; Mismatches 79; Indels 34; Gaps 12;

QY 38 VOCFVFNVEYMNCTWNSSEPOPTNLTLHYWYKNSDNDKVKQCS----HYLFSSEITSGC 93
Db 248 LECFPGAALVSCSWEVKKE-VASSVSFGLFYKPSDPAGEECSPVLREGLSLTHRHHC 306
QY 94 QLOKKEIHLHYQTFFVVLQDPRPRRQATQMLKQLNVLIPWAPENLTHLKLSQLELW 153
Db 307 QLPVPDPATHQYIVSVQ-----PRR-AEKLIK-SSVNIQWAPPSELNVTKGDS-YSLRWE 359
QY 154 NRLFNLCHLEH-----VQYRTD---WDHSWTEQSVDRHKFSLSFSDGQKRYTFVRVSR- 204
Db 360 TMMKRY--EHIDHTFEIQRYKDTATWDSKTE-TLQNAHSMALPALSPSTRYMARVRVT 416
QY 205 -----FNPCLGSAQHWSEWSPHIHWGNT 228
Db 417 SRTGYNGI-----WSEWSEARSWDTS 438

RESULT 7
JQ1655
prolactin receptor precursor - chicken
C:Species: Gallus gallus (chicken)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 28-Jul-2000
C:Accession: JQ1655
R:Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.
Biochem. Biophys. Res. Commun. 188, 490-496, 1992
A:Title: Double antenna structure of chicken prolactin receptor deduced from the cDNA se
A:Reference number: JQ1655; MUID:93075121; PMID:1445292
A:Accession: JQ1655
A:Molecule type: mRNA
A:Residues: 1-831 <TAN>
A:Cross-references: DBJ:D13154; MID:9222848; PIDN:BAA02439.1; PID:9222849
A:Experimental source: kidney
C:Superfamily: cytokine receptor homology
C:Keywords: glycoprotein; transmembrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-831/Product: prolactin receptor #status predicted <MAT>
```


A:Gene: GDB:CSF2RA; CSF2R
A:Cross-references: GDB:118777; OMIM:306250; OMIM:425000
A:Map position: Xp22.3-Xp22.32; Ipl1.3-Ipl1.3
C:Keywords: glycoprotein; growth factor receptor; transmembrane protein
F:1-2/Domain: signal sequence #status predicted <SIG>
F:23-400/Product: granulocyte-macrophage colony-stimulating factor receptor #status predicted <TM>
F:232-346/Domain: transmembrane #status predicted <TM>
F:46,54,99,123,135,182,195,223,229,272,305/Binding site: carbohydrate (Asn) (covalent) #
Query Match 11.4%; Score 146.5; DB 2; Length 400;
Best Local Similarity 21.4%; Pred. No. 0.00011;
Matches 52; Conservative 4; Mismatches 90; Indels 61; Gaps 10; #

Query Match	11.3%;	Score 145.5;	DB 2;	Length 333;
Best Local Similarity	21.1%;	Pred. No. 0.0001;		
Matches	52;	Conservative 43;	Mismatches 90;	Indels 61;
				Gaps 10
QY	5	ILTPN-GNEDTTADFFLLTMTPTDSLSVSTLPLEPVCQCFVNVEYMNCTWNSSSEPOPTKL 63		
Db	109	LLYPNSGREGTAQNF-----SCFIYNADLMNCTW-ARGPTAPRDV 148		
QY	64	TLHWYKNSDNDKVKQSHYLPSEITSGCOLQ-----KCEHLVQTFV 107		
Db	149	QYFLYIRNKKRRREIRCPYIYQDSGTWVGCHLNLSGLSRNRYLVNGTSREIGI--QFF 206		
QY	108	VOLODPRE-----PRRQATQMLKLNIVIPAPENLTLHKLS--ESQLELNWNRNFLNHC 160		
Db	207	DSLLDTKKIERFNPPSNVTRCNTHTCLVFW-KQPRTYCKLSYLDPFQYQLDVHRKNTQFG 265		
QY	161	LEHLVQYETDWDHSWTEQSVDYRHKFLPSVDGQKATTFVRSRFNPLCGSAQHWSEWH 220		
Db	266	TENLT-----INVSGLDENRYNFPSEPRKHSVKIRAADVRIL-----NWSSNSE 311		
QY	221	PIHWGS 226		
Db	312	AIEFGS 317		

RESULT 10
I56563
interleukin-3 receptor beta-subunit - rat

```
C;Species: Rattus sp. (rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 27-Oct-2003
C;Accession: I56563
R;Appel, K.; Buttini, M.; Sauter, A.; Gebicke-Haerter, P.J.
J. Neurosci. 15, 5800-5809, 1995
A;Title: Cloning of rat interleukin-3 receptor beta-subunit from cultured microglia and
A;Reference number: I56563; MUID:95370942; PMID:7643220
A;Accession: I56563
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-896 <RES>
A;Cross-references: GB:S79263; NID:gl086954; PIDN:AAB35068.1; PID:gl086955
C;Genetics:
A;Gene: IL-3Rbeta
C;Superfamily: interleukin (IL)-3/IL-5/GM-CSF receptor common beta chain; cytokine recep
C;Keywords: cytokine receptor
F;39-235/Domain: cytokine receptor homology <CRS1>
F;253-433/Domain: cytokine receptor homology <CRS2>

Query Match 10.6%; Score 136.5; DB 2; Length 896;
Best Local Similarity 23.9%; Pred. No. 0.0019;
Matches 48; Conservative 41; Mismatches 83; Indels 29; Gaps 11;

QY 38 VQCFVFNVEYMNCTWNSSEPOPTNLTLHYWYKNSDNDKVKQKSHYLFSEITSG----- 92
DB 251 LQCFPDGQSLNCSNEVNIK-VTDSVSGLFSSPKAGEKKCSFVV--RELQASRYTRY 307
QY 93 -COLQKKEIHLYQTFVVOLOQDPREPRQATQMLKQLNVLIPWAPENLTLHLKLSOLELN 151
DB 308 HCSLNVSDPAHQSQYTSVK-----RLQGRFIESFN-HIQWNPPTNLTKNRDS-YSLH 360
QY 152 WNNR-----FLNLCLEHLVOYRTD---WDHSTQSVYRKPSLPSVDGQKRYTFVRVS 203
DB 361 WETQKMSYPPFQAHQ--VQYKKLDRWEDSKTE-NLNHAHMDLPQLEPGTSCARVRV 417
QY 204 RFNPLCGSAQHWSEWSHPH 224
DB 418 KTIPEYKGL--WSEWSNCTW 436

RESULT 11
S50040
N;Alternate names: GM-CSF receptor alpha-3 chain - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999
C;Accession: S50040; S47568
R;Hu, X.; Zuckerman, K.S.
submitted to the EMBL Data Library, March 1994
A;Description: Cloning and sequencing of the cDNA encoding alternative splicing variants
A;Reference number: S50039
A;Accession: S50040
A;Molecule type: mRNA
A;Residues: 1-378 <HUX>
A;Cross-references: EMBL:L29349; NID:9460284; PIDN:AAA60962.1; PID:9463107
R;Hu, X.; Emanuel, P.D.; Zuckerman, K.S.
Biochim. Biophys. Acta 1223, 306-308, 1994
A;Title: Cloning and sequencing of the cDNA encoding two alternative splicing-derived v
A;Reference number: S47567; MUID:9436898; PMID:8086503
A;Accession: S47568
A;Molecule type: mRNA
A;Residues: 241-315,317-378 <HW>
A;Cross-references: EMBL:L29349
C;Genetics:
A;Gene: GM-CSF-RA3; CSF3RA
A;Introns: 316/3
C;Keywords: alternative splicing; glycoprotein; growth factor receptor; transmembrane pr
Query Match 10.5%; Score 135.5; DB 2; Length 378;
Best Local Similarity 20.5%; Pred. No. 0.00081;
Matches 50; Conservative 43; Mismatches 90; Indels 61; Gaps 10;

QY 5 ILTPN-GNEDTTADFFLTMTDLSVSTLPLPVCQFVFNVEYMNCTWNSSEPPQPTNL 63

Db 109 LILPNSGRETTAQNPF-----SCFIYNADLMNCTW-ARGPTAPRDV 148
QY 64 TLHYWYKNSDNDKVKQKSHYLFSEITSGCOLQ-----KKEIHLYQTFV 107
Db 149 QYELIYTRNSKRREIRCPVYIQDSGTHVCHLDNLNLSGLTSRNVFLVNGTSREIGI--QFF 206
QY 108 VOLOQDPRE-----PRQATQMLKQLNVLIPWAPENLTLHLKLS--BSOLELWNNRFLNHC 160
Db 207 DSLDTKKLERFNPPNSVNTVNTTCLVRW-KQPTYQKLSYLDQYQYQYQYQYQYQYQYQY 265
QY 161 LEHLVOYRTDWDHSTQSVYRKPSLPSVDGQKRYTFVRVSRENPLCGSAQHWSEWSH 220
Db 266 TENLL-----INVSGDLENRYNPPSSPRAKHSVKIRAADVRIL----NWSWSE 311
QY 221 PIHW 224
Db 312 AIBF 315

RESULT 12
I50455
prolactin receptor - pigeon
C;Species: Columba livia (domestic pigeon)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 28-Jul-2000
C;Accession: I50455
R;Chen, X.; Horseman, N.D.
Endocrinology 135, 269-276, 1994
A;Title: Cloning, expression, and mutational analysis of the pigeon prolactin receptor.
A;Reference number: I50455; MUID:94283267; PMID:7516866
A;Accession: I50455
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-830 <CHE>
A;Cross-references: EMBL:U07694; NID:9466381; PIDN:AAA20646.1; PID:9466382
C;Superfamily: cytokine receptor homology
F;36-220/Domain: cytokine receptor homology <CRS1>
F;240-426/Domain: cytokine receptor homology <CRS2>

Query Match 10.3%; Score 132.5; DB 2; Length 830;
Best Local Similarity 22.2%; Pred. No. 0.0037;
Matches 44; Conservative 37; Mismatches 96; Indels 21; Gaps 7;

QY 38 VQCFVFNVEYMNCTWNSSE-POPTNLTLHYWYKNSDNDKVKQKSHYLFSEITSGCOLQ 96
Db 34 ICRSLKLEKTFSCWKPQSGDGLPTNYTL--FYSKDSEKIYECPDYQMSG--PNSCYFD 89
QY 97 KKEIHLYQTFVVOLOQDPREPRQAT--QMLKQLNVLIPWAPENLTLH---KLSSOLELN 151
Db 90 KNTNPWTITNYITVAMNEIGNSSDPQYVDVTSIVQPDAPVNLSTETKSASTYLLAK 149
QY 152 WNNRFL-----NHCLEHLVOYRTDWDHSTQSVYRKPSLPSVDGQKRYTFVRSRF 205
Db 150 WSPFPPLADVTSNHYRYELRLKPEKEWETVSGVQYQYQYQYQYQYQYQYQYQYQY 209
QY 206 NPLCGSAQHWSEWSHPH 223
Db 210 D-----IGWSEWSSERH 222

RESULT 13
A33380
interleukin-4 receptor precursor - mouse
N;Alternate names: IL-4 receptor
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 01-Dec-2000
R;Mosley, B.; Beckmann, M.P.; March, C.J.; Idzerda, R.L.; Gimpel, S.D.; VandenBos, T.; F
Widmer, M.B.; Cosman, D.; Park, L.S.
Cell 59, 335-348, 1989
A;Title: The murine interleukin-4 receptor: molecular cloning and characterization of se
A;Reference number: A30911; MUID:90030408; PMID:2805066
A;Accession: A33380
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A;Molecule type: mRNA
A;Residues: 1-810 <MOI>
A;Cross-references: GB:M27959; NID:G198363; PIDN:AAA39299.1; PID:G309408
A;Accession: B33380
A;Molecule type: mRNA
A;Residues: 1-258 <MO2>
A;Accession: C33380
A;Molecule type: mRNA
A;Residues: 1-224, 'PSNENL' <MO3>
A;Cross-references: GB:M27960; NID:G198365; PIDN:AAA39300.1; PID:G309409
A;Note: part of this sequence, including the amino end of the mature protein, was confirmed by three forms of cDNA were isolated; the longest encodes extracellular, transmembrane domain and may encode a soluble form of the receptor
A;Harada, N.; Castle, B.E.; Gorman, D.M.; Itoh, N.; Schreurs, J.; Barrett, R.L.; Howard, Proc. Natl. Acad. Sci. U.S.A. 87, 857-861, 1990
A;Title: Expression cloning of a cDNA encoding the murine interleukin 4 receptor based on A;Reference number: A34861; MUID:90138976; PMID:2405398
A;Accession: A34861
A;Molecule type: mRNA
A;Residues: 1-810 <HAR>
A;Cross-references: GB:M29854; NID:G198346; PIDN:AAA39297.1; PID:G309407
A;Wrighton, N.C.; Campbell, L.A.; Lee, F.D.
Growth Factors 6, 103-118, 1992
A;Title: The murine interleukin-4 receptor gene: Genomic structure, expression and potential A;Reference number: I54232; MUID:92265335; PMID:1534014
A;Accession: I54232
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-73, '1', 75-333, 'P', 335-810 <RES>
A;Cross-references: GB:M64879; NID:G198359; PIDN:AA59727.1; PID:G198361
C;Genetics:
A;Insertions: 24/1; 71/2; 122/1; 172/3; 225/1; 258/2; 284/3; 301/2
A;Superfamily: interleukin-4 receptor; cytokine receptor homology
C;Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane protein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-810/Product: interleukin-4 receptor #status experimental <MAT>
F;26-233/Domain: extracellular #status predicted <EXT>
F;24-219/Domain: cytokine receptor homology <CRS>
F;234-257/Domain: transmembrane #status predicted <TM>
F;258-810/Domain: intracellular #status predicted <INT>
F;72,129,135,163,177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.2%; Score 132; DB 1; Length 810;
Best Local Similarity 26.2%; Pred. No. 0.004;
Matches 60; Conservative 28; Mismatches 107; Indels 34; Gaps 8;

QY 14 TTADPFLTMTPTDLSVSTLPPEVQCFVFNVEYNNCTW--NSSSEPOPTNLTLHYWYKNS 72
DB 10 TSVGCLILLVTGSGIKVLGEP--TCPSDYRTSTCEWFLDSDAVDCSSQLCLHY----- 62
QY 73 DNDKVKQCSHYLFSSEIT-----SCQLOKKEIHLVQTFVVLQDPREPRQATQML 124
DB 63 -----RLMFFESNLTICIPRNSASTVCVCHMENRNPVQSDRYQMELWAEHRLWQGSF 116
QY 125 KLQNLVLPWAPENLTLKLSESLQELNWNFLNHL--EHLVQY---RTDWDHSWTEQ 178
DB 117 SPFGNVKPLADPNLTLHTNVSDWLTLWNLYPSNNLLYKDLISWNISREDNPAEFIVY 176
QY 179 SVDY---RHKFLSPVDGQKRYTFRVRSPFNPLCGSAGHWSHPIHW 224
DB 177 NVTYKEPLSPFNILMGSGVYVYARVRSQILTGT---WSESPSITW 222

RESULT 14
A35782
Cytokine receptor common beta chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 27-Oct-2003
C;Accession: A35782
R;Gorman, D.M.; Itoh, N.; Kitamura, T.; Schreurs, J.; Yonehara, S.; Yahara, I.; Arai, K. Proc. Natl. Acad. Sci. U.S.A. 87, 5459-5463, 1990
A;Title: Cloning and expression of a gene encoding an interleukin 3 receptor-like protein
A;Reference number: A35782; MUID:90139131; PMID:1695379

A;Accession: A35782
A;Molecule type: mRNA
A;Residues: 1-896 <GOR>
A;Cross-references: GB:M34397; NID:G191821; PIDN:AAA37204.1; PID:G309101
C;Comment: Mouse high-affinity IL-5, GM-CSF, and one class of high-affinity IL-3 receptor
C;Superfamily: interleukin (IL)-3/IL-5/GM-CSF receptor common beta chain; cytokine receptor
C;Keywords: cytokine receptor; duplication; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-896/Product: cytokine receptor common beta chain #status predicted <MAT>
F;23-441/Domain: extracellular #status predicted <EXT>
F;239-235/Domain: cytokine receptor homology <CRS1>
F;253-434/Domain: cytokine receptor homology <CRS2>
F;442-463/Domain: transmembrane #status predicted <TM>
F;464-896/Domain: intracellular #status predicted <INT>

Query Match 9.7%; Score 125; DB 1; Length 896;
Best Local Similarity 23.1%; Pred. No. 0.017; Indels 42; Gaps 11;
Matches 48; Conservative 36; Mismatches 82;

QY 38 VOCFVFNVEYNNCTWSSSEPPQPTNLTLHYWYKNSDNDKVKQCSHYLFSSEITSGCQLQK 97
DB 251 LQCFPDGIGSLHCSMEVWTQ--TTGVSFGLFYRSPVAPBEKCSPV----- 296
QY 98 KE---LHLYQYFVVLQDPREPRQATQMLKQLNV-----IPWAPENLTLHLKLS 144
DB 297 YPFRVRSFNPLCGSAGHWSHPIHW 224
QY 145 ESQLELNWNR-----FLNHLCHLHVQY---TMDHSWTEQSVQVYRHKFLSPVDGQKR 196
DB 356 DS--YSLHWETQKWAYSFIEHTFQ--VOYKKKSDSWEDSKTE--NLDRAHSMDSLQLEPDT 411
QY 197 YPFRVRSFNPLCGSAGHWSHPIHW 224
DB 412 YCARVRVK--PISNYDGIWSKWSSEYTW 437

RESULT 15
I45971
Prolactin receptor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 28-Jul-2000
C;Accession: I45971
R;Scott, P.; Kessler, M.A.; Schuler, L.A.
Mol. Cell. Endocrinol. 89, 47-58, 1992
A;Title: Molecular cloning of the bovine prolactin receptor and distribution of prolactin A;Reference number: I45971; MUID:93246019; PMID:1338725
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-581 <SCO>
A;Cross-references: GB:L02549; NID:G163617; PIDN:AAA51417.1; PID:G163618
C;Genetics:
A;Gene: PRLR
C;Superfamily: cytokine receptor homology
F;36-221/Domain: cytokine receptor homology <CRS>

Query Match 9.4%; Score 121.5; DB 2; Length 581;
Best Local Similarity 25.4%; Pred. No. 0.02;
Matches 60; Conservative 30; Mismatches 69; Indels 77; Gaps 17;

QY 28 LSVSTL---PLPE---VQCFVFNVEYNNCTWSSSE--PQPTNLTLHYWYKNSDNDKVKQ 79
DB 17 LSVSLNGQSPPEKPLVKCRSPGKETTCWPEAGDGLPNTYLTLY--HKEGT-LIHE 74
QY 80 CSHYLFSEBITSG---CQLOKKEIHLVQTFVVLQ-----ODPR-----EPRR 118
DB 75 CPDYK-----TGPNSCYFSGKHTSIWKWYVITVNAIQMGISSSDPLVYVHVYIPEPEP 129
QY 119 QATQMLKLN-----LVIPWAPENLTLKLSESLQELNWNFLNHLCHLHVQY--- 168
DB 130 PANLTLELHPEDRPFYIKWSPPTMT-----DVKSGW-----FIQYFRL 172
QY 169 -----TMDHSWTEQSVQVYRHKFLSPVDGQKRYTFRVRSFNPLCGSAGHWSHWS 219

Db 173 KPEKATDWEHTLTKOTLK-IFNL--YFGQK---YLVQIRCKPDHG---YWEWS 219

Search completed: March 3, 2004, 12:38:59
Job time : 16.5425 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 3, 2004, 12:31:14 ; Search time 37.9085 Seconds
(without alignments)
1930.971 Million cell updates/sec

Title: US-09-825-561A-4

Perfect score: 1288

Sequence: 1 LNTLTLPNGNEDTTADFFL.....QHWSESHPIHWSNTSKEN 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mmc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	997.5	77.4	368	Q8SQ71	Q8sq71 sus scrofa
2	919	71.4	278	Q8VHR8	Q8vhr8 rattus norv
3	667.5	51.8	448	Q7TP53	Q7tp53 rattus norv
4	427.5	33.2	348	Q8AUP2	Q8aup2 gallus gall
5	427.5	33.2	374	Q8AV07	Q8av07 gallus gall
6	283.5	22.0	343	Q9DRQ1	Q9deq1 oncorhynch
7	273.5	21.7	313	Q8JJD1	Q8jjd1 oncorhynch
8	253.5	20.1	404	Q90AP8	Q90ap8 oncorhynch
9	213	16.5	386	Q95LFO	Q95lfo canis fami
10	204.5	15.9	385	Q8VHK6	Q8vhk6 rattus norv
11	193.5	15.5	383	Q8VHK6	Q8vhk6 mus musculu
12	183.5	14.2	424	Q8BNM4	Q8bnm4 mus musculu
13	181.5	14.1	424	Q8C1Z3	Q8c1z3 mus musculu
14	181.5	14.1	442	Q7TT27	Q7tt27 mus musculu
15	178	13.8	427	Q96BB4	Q96bb4 homo sapien
16	177	13.7	409	Q7YRV5	Q7yrv5 macaca fasc

17	172.5	13.4	405	6	Q95LFI	Q95lfi canis fami
18	169.5	13.2	426	11	Q8VHC2	Q8vhc2 rattus norv
19	159.5	12.4	371	4	Q9HC73	Q9hc73 homo sapien
20	154.5	12.0	423	6	Q8G3Z6	Q8g3z6 sus scrofa
21	150	11.6	460	13	Q7T2Z0	Q7t2z0 gallus gall
22	141.5	11.0	249	4	Q8WX09	Q8wx09 homo sapien
23	141.5	11.0	279	4	Q9UDY5	Q9udy5 homo sapien
24	139	10.8	890	11	Q9Z1A0	Q9z1a0 cavia porce
25	137.5	10.7	415	11	Q9Z0X4	Q9z0x4 cavia porce
26	137.5	10.7	881	13	Q57519	Q57519 xenopus lae
27	137	10.6	349	6	Q97597	Q97597 bos taurus
28	136.5	10.6	896	11	Q64146	Q64146 rattus norv
29	136	10.6	232	4	Q9H5R3	Q9h5r3 homo sapien
30	132.5	10.3	896	11	Q8QZX9	Q8qzx9 mus musculu
31	132	10.2	810	11	Q8CBW5	Q8cbw5 mus musculu
32	130	10.1	611	13	Q9IBF6	Q9ibf6 xenopus lae
33	130	10.1	611	13	Q9PTI0	Q9pti0 xenopus lae
34	130	10.1	810	11	Q54690	Q54690 mus musculu
35	128	9.9	810	11	Q60583	Q60583 mus musculu
36	125	9.7	611	13	Q9PTH9	Q9pth9 xenopus lae
37	124.5	9.7	918	13	Q9W6U9	Q9w6u9 gallus gall
38	120.5	9.4	229	11	Q9RLW8	Q9rlw8 rattus norv
39	120.5	9.4	801	11	Q9WTM8	Q9wtm8 rattus norv
40	119.5	9.3	800	11	Q63257	Q63257 rattus norv
41	118.5	9.2	359	11	Q8CII9	Q8cii9 mus musculu
42	118.5	9.2	370	11	Q9JIO7	Q9jio7 mus musculu
43	117.5	9.1	359	11	Q9JMD5	Q9jmd5 mus musculu
44	117.5	9.1	809	6	Q8MIR9	Q8mir9 equus cabal
45	116.5	9.0	359	11	Q9UJH8	Q9ujh8 mus musculu

ALIGNMENTS

RESULT 1

Q8SQ71 ID Q8SQ71 PRELIMINARY; PRT; 368 AA.
AC Q8SQ71;
DT 01-JUN-2002 (TREMREL. 21, Created)
DT 01-JUN-2002 (TREMREL. 21, Last sequence update)
DT 01-OCT-2003 (TREMREL. 25, Last annotation update)
DE Interleukin 2 receptor gamma.
GN IL2RG.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Splice;
RA Uenishi H.;
RT "Molecular cloning of porcine interleukin 2 receptor gamma."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB040442; BAB86592.1;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . . ; IEA.
DR GO; GO:0004872; F:receptor activity; IEA
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR003531; Hemopoetin_s_F1.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
SQ SEQUENCE 368 AA; 41810 MW; 43643AB0741ADFD7 CRC64;

Query Match 77.4%; Score 997.5; DB 6; Length 368;

Best Local Similarity 78.9%; Pred NC 4.5e-86;

Matches 193; Conservative 18; Mismatches 30; Indels 1; Gaps 1;

QY 1 LNTLTLPNGNEDTTADFFLTTMPDLSVSLFLPEVQCFFVFNVMNCTWNSSSPQP.60

```

Db 23 LNPXVLTSGNEDITADFLLLSTPOTLNVSTLPLPKVQCFVFNVEYVNCVTWNSSELQP 82
QY 61 TNLTHYWKNSNDKVKQKSHYLFSEETISGQLOKKEIHLYQTFVVOLODPPRROA 120
Db 83 TNLTHYWKNSNDKVKQKSHYLFSEETISGQLOKKEIHLYQTFVVOLODPPRROD 142
QY 121 TQMLKQNLVLPWAPENLTLHLKLSQLELNWNNRFLNCHLHLYQYRTDWDHSTEQSV 180
Db 143 PQTLKQDLVLPWAPENLTLHLKLSQLELNWNNRFLNCHLHLYQYRTDWDHSTEQSV 202
QY 181 DYHKSFLPSVDQKRYTFRVRSRNPFLCGSAQHWSEWSPHIHWSNTSKEN 232
Db 203 DHRQSFSLPSVDAQLYTFRVRSRNPFLCGSAQHWSEWSPHIHWSNTSKEN 253

RESULT 2
Q8VHR8 PRELIMINARY; PRT; 278 AA.
AC Q8VHR8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cytokine receptor gamma chain (Fragment).
GN IL2RG.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Oloz F., Malek T.R.;
RA Chai L.Q., Yuan J.Y., Yang K.J., Yan H.M., Chang C.F., Zhao L.F.,
RA Ma H., Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;
RT "Liver regeneration after PH.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY325195; AAP92596.1; -.
DR EMBL; AY325195; AAP92596.1; -.
SQ SEQUENCE 278 AA; 51863 MW; EBD56D1FA86614D5 CRC64;

Query Match 71.4%; Score 919; DB 11; Length 278;
Best Local Similarity 70.6%; Pred. No. 8.6e-79;
Matches 163; Conservative 33; Mismatches 35; Indels 0; Gaps 0;

QY 2 NNTLTTPNGNEDTADFFLTMTDLSVSTLPLPEVQCFVFNVEYVNCVTWNSSEPOPT 61
Db 2 SSKVLLSSNGNETKSDLLTSDMLKLSVPTLPLPEVQCFVFNVEYVNCVTWNSSEPOPT 61
QY 62 NTLTHYWKNSNDKVKQKSHYLFSEETISGQLOKKEIHLYQTFVVOLODPPRROAT 121
Db 62 NLTMYRYKSGSDNTFQECGSHYLFSEETISGQLOKKEIHLYQTFVVOLODPPRRAE 121
QY 122 QMLKQNLVLPWAPENLTLHLKLSQLELNWNNRFLNCHLHLYQYRTDWDHSTEQSV 181
Db 122 QMLKQNLVLPWAPENLTLHLKLSQLELNWNNRFLNCHLHLYQYRTDWDHSTEQSV 181
QY 182 YHKSFLPSVDQKRYTFRVRSRNPFLCGSAQHWSEWSPHIHWSNTSKEN 232
Db 182 HEPFSLPSVDQKLYTFRVRSRNPFLCGSTQWKSQPIHWSHTAEEN 232

RESULT 3
Q7TP53 PRELIMINARY; PRT; 448 AA.
AC Q7TP53;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ab2-183.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Xu C.S., Li W.Q., Li Y.C., Wang L., Wang S.F., Han H.P., Wang G.P.,
RA Chai L.Q., Yuan J.Y., Yang K.J., Yan H.M., Chang C.F., Zhao L.F.,
RA Ma H., Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;
RT "Liver regeneration after PH.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY325195; AAP92596.1; -.
DR EMBL; AY325195; AAP92596.1; -.
SQ SEQUENCE 448 AA; 51863 MW; EBD56D1FA86614D5 CRC64;

Query Match 51.8%; Score 667.5; DB 11; Length 448;
Best Local Similarity 70.2%; Pred. No. 9.2e-55;
Matches 118; Conservative 26; Mismatches 23; Indels 1; Gaps 1;

QY 66 HYV-YXNSDNDKVKQKSHYLFSEETISGQLOKKEIHLYQTFVVOLODPPRROATQML 124
Db 21 HDWRYKSGSDNTFQECGSHYLFSEETISGQLOKKEIHLYQTFVVOLODPPRRAEOKL 80
QY 125 KQNLVLPWAPENLTLHLKLSQLELNWNNRFLNCHLHLYQYRTDWDHSTEQSV 184
Db 81 NLQNLVLPWAPENLTLHLKLSQLELNWNNRFLNCHLHLYQYRTDWDHSTEQSV 140
QY 185 KFLPSVDQKRYTFRVRSRNPFLCGSAQHWSEWSPHIHWSNTSKEN 232
Db 141 RFLPSVDQKLYTFRVRSRNPFLCGSTQWKSQPIHWSHTAEEN 188

RESULT 4
Q8AUP2 PRELIMINARY; PRT; 348 AA.
AC Q8AUP2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative common cytokine receptor gamma chain a precursor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=white leghorn SC, and Leghorn; TISSUE=Liver, and Spleen;
RX MEDLINE=22325486; PubMed=12437989;
RA Min W., Lillehoj H.S., Fetterer R.H.;
RT "Identification of an alternatively spliced isoform of the common
RT cytokine receptor gamma, Greek chain in chickens.";
RL Biochem. Biophys. Res. Commun. 299:321-327(2002).
DR EMBL; AJ419897; CAD12042.1; -.
DR EMBL; AJ419898; CAD12043.1; -.
DR PIR; JC7907; JC7907.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR003531; Hemtopoptn_S_F1.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
DR Receptor; Signal.
FT SIGNAL 1 21 POTENTIAL
SQ SEQUENCE 348 AA; 39750 MW; 93DEC9F15DE9BBE6 CRC64;

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Query Match 33.2%; Score 427.5; DB 13; Length 348;
Best Local Similarity 42.9%; Pred. No. 3.4e-32;
Matches 91; Conservative 36; Mismatches 56; Indels 29; Gaps 9;

QY 34 PLPE-VQCFVFNVEYMNCTWSSSPQPTNLTLYWYKNSDNDKVKCKSHYLFSEETSG 92
DB 24 PSPKGVECLFNEEYMTCTW-GSGQTLTANYSLYYWEN--KLPVVEQQYLWDRSVRIG 80
QY 93 COLQKEIHLVYTFVQ-----LQDPREPRAQATQMLKQLNVLIPWAPENLTLHLK 143
DB 81 CRFQSEIIFQAFYRVNASCNGQTLP-----SNRMELQNLVKPEAPVNLTHNM 133
QY 144 SESQLELNNRRF-LNHCHLEHLVQRTDWDHSWTEQSDVYRHK---FSLPSVDGQKTYTF 199
DB 134 SGNQLQLTWSSPYPKQCLEHVKYKSKNDTSWNTQEV----KGVIFSPFSDYKTYTF 189
QY 200 RYRSRPNPLCGSAQHSWSHPHWSN-TSK 230
DB 190 YVRSKINNYCGNTQLWSEWSVFWGNNSTSK 221

RESULT 5
QYAV07 PRELIMINARY; PRT; 374 AA.
AC Q8AV07;
DT 01-MAR-2003 (TREMELrel. 23, Created)
DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Putative common cytokine receptor gamma chain b precursor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=white leghorn SC; TISSUE=Spleen;
RX MEDLINE=2325486; PubMed=12437989;
RA Min W., Lillehoj H.S., Fetterer R.H.;
RT "Identification of an alternatively spliced isoform of the common
RT cytokine receptor gamma, Greek chain in chickens."
RL Biochem. Biophys. Res. Commun. 299:321-327(2002).
DR EMBL; AJ419896; CAD12041.1;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN.III.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
KW Signal; Receptor.
FT SIGNAL
SQ SEQUENCE 374 AA; 42547 MW; B3A62E0D4D02B42B CRC64;

Query Match 33.2%; Score 427.5; DB 13; Length 374;
Best Local Similarity 42.9%; Pred. No. 3.7e-32;
Matches 91; Conservative 36; Mismatches 56; Indels 29; Gaps 9;

QY 34 PLPE-VQCFVFNVEYMNCTWSSSPQPTNLTLYWYKNSDNDKVKCKSHYLFSEETSG 92
DB 24 PSPKGVECLFNEEYMTCTW-GSGQTLTANYSLYYWEN--KLPVVEQQYLWDRSVRIG 80
QY 93 COLQKEIHLVYTFVQ-----LQDPREPRAQATQMLKQLNVLIPWAPENLTLHLK 143
DB 81 CRFQSEIIFQAFYRVNASCNGQTLP-----SNRMELQNLVKPEAPVNLTHNM 133
QY 144 SESQLELNNRRF-LNHCHLEHLVQRTDWDHSWTEQSDVYRHK---FSLPSVDGQKTYTF 199
DB 134 SGNQLQLTWSSPYPKQCLEHVKYKSKNDTSWNTQEV----KGVIFSPFSDYKTYTF 189
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QY 200 RYRSRPNPLCGSAQHSWSHPHWSN-TSK 230
DB 190 YVRSKINNYCGNTQLWSEWSVFWGNNSTSK 221

RESULT 6
QYDEQ1 PRELIMINARY; PRT; 343 AA.
AC Q9DEQ1;
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Cytokine receptor common gamma chain.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21287902; PubMed=11394690;
RA Wang T., Secombes C.J.;
RT "Cloning and expression of a putative common cytokine receptor gamma
RT chain gene in rainbow trout (Oncorhynchus mykiss).";
RL Fish and Shellfish Immunol. 11:233-244(2001).
DR EMBL; AJ276623; CAC09429.2;
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003961; FN.III.
DR SMART; SM00060; FN3; 1.
KW Receptor.
SQ SEQUENCE 343 AA; 39486 MW; ED8429E7534B21EB CRC64;

Query Match 22.0%; Score 283.5; DB 13; Length 343;
Best Local Similarity 30.9%; Pred. No. 1.4e-18;
Matches 59; Conservative 37; Mismatches 88; Indels 7; Gaps 4;

QY 36 PEVQCFVFNVEYMNCTWSSSPQPTNLTLYWYKNSDNDKVKCKSHYLFSEETSG 95
DB 23 PNVNCLINLDVNCIWSQSIPE-VNFT--FFSSRFKDNMECTTYLQESYAVGRL 79
QY 96 OKKEIHLVYTFVQDPREPRAQATQMLKQLNVLIPWAPENLTLHLKSEQLNWNRR 155
DB 80 SYDKSDRFRTLTKLV---HQNNSVYVDHNLKSMVKLYPPVNLVEMNKDPELNLNNS 136
QY 156 FLNHCHLEHLVQRTDWDHSWTEQSDVYRHKSLPSVDGQKTYTFVRSRPNPLCGSAQHM 215
DB 137 KNTFIESEVRYRNSD-KWKTSTPESQKQYAVAPLKSRYEFOVARVNDMCGSEFW 195
QY 216 SEWSHPHWS 226
DB 196 SEWSQPIQWDS 206

RESULT 7
Q8JJD1 PRELIMINARY; PRT; 313 AA.
AC Q8JJD1;
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Cytokine receptor common gamma chain precursor.
GN IL2RGAMMA.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA Soma G., Inagawa H., Honda T., Nishizawa T., Kanou J., Endo M.,
RA Ootake M., Nakanishi T.;
RT "Rainbow trout cytokine receptor common gamma chain precursor (IL-2R
RT gamma chain) like protein.";
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RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB042024; BAB91242.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Signal; Receptor.
FT SIGNAL.
SQ SEQUENCE 313 AA; 36259 MW; 28278777AF2F9BF2 CRC64;
    Query Match      21.7%; Score 279.5; DB 13; Length 313;
    Best Local Similarity 30.4%; Pred. No. 2.9e-18;
    Matches 58; Conservative 38; Mismatches 88; Indels 7; Gaps 4;
    QY 36 PFVQCFVFNVEYVNCWNSSEPPQTNLTLYHYKNSDNDKVKCSHYLFSFEETSGCOL 95
    Db 23 PNVCCLINLVNCIWSQSIPV-VNFT--PFSSRFKIDNMEECTTYLQDSVAVGCL 79
    QY 96 OKKEIHLVQTFVVLQODPREPRQATOMLKLQNLVTPWAPENILTLKLSQLELNNR 155
    Db 80 SYDKSDRFILTKLV---HQMSTVQDHNLKSMVKLYPPVNLSEVMNKDPELNDYNN 136
    QY 156 FLNHGLEHLVQYRTDWDHBSWTEQSDYDRHKFSLPSVDGQKRYTFVRSRFPLCGSAQHW 215
    Db 137 KNTFCIESEVRVIRNSD-KWKTSTFSEKQYAVAFPLKSRVFEQVRAVRNDMCGESKF 195
    QY 216 SEWSHPIHWS 226
    Db 196 SEWSQPIQWDS 206
    RESULT 8
    Q90XP8 PRELIMINARY; PRT; 404 AA.
    AC Q90XP8;
    DT 01-DEC-2001 (Tremblrel. 19, Created)
    DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
    DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
    DE Interleukin 13 receptor alpha-2.
    OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
    OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
    OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
    OX NCBI_TaxID=8022;
    RN [1]
    RP SEQUENCE FROM N.A.
    RA Lockyer A.E., Jones C.S., Noble L.R., Verspoor E., Holland J.,
    RA Secombes C.J.;
    RT "Isolation and characterization of a putative interleukin 13 receptor
    RT alpha-2 sequence from rainbow trout (Oncorhynchus mykiss).";
    RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
    DR EMBL; AF361437; AAL26927.1; -.
    DR GO; GO:0004872; F:receptor activity; IEA.
    DR InterPro; IPR002996; CRIA.
    DR InterPro; IPR008957; FN_III-like.
    KW Receptor.
    SQ SEQUENCE 404 AA; 46728 MW; 4B9B7E3F4CFFB6D6 CRC64;
    Query Match      20.1%; Score 259.5; DB 13; Length 404;
    Best Local Similarity 27.9%; Pred. No. 3.1e-16;
    Matches 56; Conservative 44; Mismatches 88; Indels 13; Gaps 6;
    QY 40 CFVFNVEYVNCWNSSEPPQTNLTLYHYKNSDNDKVKCSHYLFSFEETSGCOLQKK 98
    Db 143 CVFYKFEFMECTWETGLEPFSQSYLFWHR--EMEQABECPQYIHNGVRTGCKFTEE 200
    QY 99 ETHLYQTF--VVLQODPREPRQATOMLKLQNLVTPWAPENILTLKLSQLELNNW--N 153
    Db 201 SUSEFDFNICNSSPEVVLASAFSLQIQNYVFALETVHLASDRLQVQWDLPN 260
    QY 154 NRLFNLCHLEHLVQYRTD--WDHSWTEQSDYDRHKFSLPSVDGQKRYTFVRSRFPLCGS 211
    Db 261 ERIPRCHLEVEAREEGVGQGPLLQRTVNTNEMTLTSLMSDGAARKCFVRVSRMHYCAD 320
    QY 212 AQHSEWSHPIHWSNTSKEN 232
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Db 321 RGFWSDWMS---HWSCHSDTES 338
    RESULT 9
    Q95LFO PRELIMINARY; PRT; 386 AA.
    AC Q95LFO;
    DT 01-DSC-2001 (Tremblrel. 19, Created)
    DT 01-DSC-2001 (Tremblrel. 19, Last sequence update)
    DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
    DE Interleukin 13 receptor alpha chain 2.
    GN IL13RA2.
    OS Canis familiaris (Dog).
    OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
    OX NCBI_TaxID=9615;
    RN [1]
    RP SEQUENCE FROM N.A.
    RA Tang L.;
    RA MEDLINE=21287533; PubMed=11389954;
    RT "Molecular cloning of canine IL-13 receptor alpha chain (alpa1 and
    RT alpa2) cDNAs and detection of corresponding mRNAs in canine
    RT tissues.";
    RL Vet. Immunol. Immunopathol. 79:181-195(2001).
    DR EMBL; AF314533; AAL14887.1; -.
    DR GO; GO:0016020; C:membrane; IEA.
    DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. .; IEA.
    DR GO; GO:0004872; F:receptor activity; IEA.
    DR InterPro; IPR002996; CRIA.
    DR InterPro; IPR008957; FN_III-like.
    DR InterPro; IPR003532; Hemopoetin_S_F2.
    DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
    KW Receptor.
    SQ SEQUENCE 386 AA; 45110 MW; AL6FDF2DD023ED95 CRC64;
    Query Match      16.5%; Score 213; DB 6; Length 386;
    Best Local Similarity 25.8%; Pred. No. 7.3e-12;
    Matches 61; Conservative 38; Mismatches 107; Indels 30; Gaps 8;
    QY 3 TTILT-PNGNEDTADFFLTMTPTDSLSVSTPLPEVQCFVFNVEYVNCWNSSEPPQ-P 60
    Db 125 TTYTSPQGNRET-----KIDMDCVYNNQYLVCSKPGMGVHFD 165
    QY 61 TNLTLHYWYKNSDNDKVKCSHYLFSFEETSGCOLQKKIHLVQYFVQLQDPRE--PRR 118
    Db 166 TNYQLFWTEGLDHS--AECTYIKVNGKMGCRPYLESSDYKDFYICVNGSSSQPIR 223
    QY 119 QATQMLKLQNLVTPWAPENILTLKLSQLELNNW---NRLFNLCHLEHLVQYRTDWDHWS 175
    Db 224 PSYFIFQLQNLVTPWAPENILTLKLSQLELNNWPKGPIPAKCFIYEIETED-GTTW 282
    QY 176 TEQSDYRHKFSLPSVDGQKRYTFVRSRFPLCGSAQHSEWSHPIHWSNTSKE 231
    Db 283 VTTVNEIQTITSNESQK-LCFLVRSKNYIYCSDDGIWSSEDEQCKWGDINKE 337
    RESULT 10
    Q8VHK6 PRELIMINARY; PRT; 385 AA.
    AC Q8VHK6;
    DT 01-MAR-2002 (Tremblrel. 20, Created)
    DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
    DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
    DE Interleukin 13 receptor alpha chain 2.
    GN IL13RA2.
    OS Rattus norvegicus (Rat).
    OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
    OX NCBI_TaxID=10116;
    RN [1]
    RP SEQUENCE FROM N.A.
    RA STRAIN=Sprague-Dawley;
    RA Wu A., Low W.C.;
```


RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.M., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Joquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skalka U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC052425; AAH52425.1; -
KW Hypothetical protein.
FT NON TER
SQ SEQUENCE 442 AA; 50128 MW; E2EF7C84C450661B CRC64;
Query Match 14.1%; Score 181.5; DB 11; Length 442;
Best Local Similarity 27.6%; Pred. No. 8.2e-09;
Matches 56; Conservative 38; Mismatches 86; Indels 23; Gaps 9;
QY 37 EVQCFVNEVMNCWNSSSEPOP-TNLTLYWYKNSDNDKVKCSH-YLFSEETSGCQ 94
DB 147 ELKCIWNLNLSYMKCSWLPGRNTSPDTHLYWY--SSLEKRGQCNITREGQHACSFK 204
QY 95 LQKKEIHL-YQTFVVOLODPRPRROATQMLKQNLVWPAPENLTJHKLSESOLELNN 153
DB 205 LTKVPSFEHQNVQIMVKDNAGKIRPSCKIVSLSYVKP-DPPHKKLLKNGALLVQWK 263
QY 154 N--RFLNHCLEHLVQY---RTD-----WDHSWTEQSDVYRHKESLPSVDGQKRY 197
DB 264 NPNFRSRCLTYEVEVNTQTDHNLILEVEDKQCNSEDRNMEGTCFQLPGLADAVY 323
QY 198 TFRVRSRNPCL-SSAOWHSEWS 219
DB 324 TVRVKTKNLCFDNDKLSWDS 346
RESULT 15
Q96BB4 PRELIMINARY; PRT; 427 AA.
AC Q96BB4; OSWK08;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Interleukin 13 receptor, alpha 1 (BB12804.2.1)
GN IL13RA1
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 31-427 FROM N.A.
RA Lawlor S.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.M., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Joquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skalka U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC052425; AAH52425.1; -
KW Hypothetical protein.
FT NON TER
SQ SEQUENCE 442 AA; 50128 MW; E2EF7C84C450661B CRC64;
Query Match 14.1%; Score 181.5; DB 11; Length 442;
Best Local Similarity 27.6%; Pred. No. 7.8e-09;
Matches 56; Conservative 38; Mismatches 86; Indels 23; Gaps 9;
QY 37 EVQCFVNEVMNCWNSSSEPOP-TNLTLYWYKNSDNDKVKCSH-YLFSEETSGCQ 94
DB 129 ELKCIWNLNLSYMKCSWLPGRNTSPDTHLYWY--SSLEKRGQCNITREGQHACSFK 186
QY 95 LQKKEIHL-YQTFVVOLODPRPRROATQMLKQNLVWPAPENLTJHKLSESOLELNN 153
DB 187 LTKVPSFEHQNVQIMVKDNAGKIRPSCKIVSLSYVKP-DPPHKKLLKNGALLVQWK 245
QY 154 N--RFLNHCLEHLVQY---RTD-----WDHSWTEQSDVYRHKESLPSVDGQKRY 197
DB 246 NPNFRSRCLTYEVEVNTQTDHNLILEVEDKQCNSEDRNMEGTCFQLPGLADAVY 305
QY 198 TFRVRSRNPCL-SSAOWHSEWS 219
DB 306 TVRVKTKNLCFDNDKLSWDS 328
RESULT 14
Q7TT27 PRELIMINARY; PRT; 442 AA.
AC Q7TT27
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment)
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

>R EMBL; BC015768; AAH15768.1; -
>R EMBL; AL391280; CAD21446.1; -
>R GO; GO:0016020; C:membrane; IEA.
>R GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
>R GO; GO:0004872; F:receptor activity; IEA.
>R InterPro; IPR002996; CR1A.
>R InterPro; IPR008957; FN_III-like.
>R InterPro; IPR003532; Hemtopoptn_S_F2.
>R PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
>W Receptor.
>Q SEQUENCE 427 AA; 48676 MW; E6A42F7466A39A09 CRC64;

Query Match 13.8%; Score 178; DB 4; Length 427;
Best Local Similarity 26.7%; Pred. No. 1.7e-08;
Matches 58; Conservative 38; Mismatches 83; Indels 38; Gaps 11;

>Y 37 EVQCFVNFVEYMNCTWNSSEPOF--TNLTLYWYKNSDNDKVKCKSHYLFSEITSGC-- 93
>B 131 ELQCIWHNLSYMKCSWLPGRNTSPDNTLYYWHRSI--EKIHQCEN--IFREGQYFGCSF 187
>Y 94 QLOKKEIHLVQTFVQL--QDPREPRQATOMLKLQNLVIPWAP--ENLTLHKLSESOLE 149
>B 188 DLTAKVDSSEFQESVQIMVKDNAGIKKPSFNIVPLTSRVKPPDPPIKNIASFH---NDDL 244
>Y 150 LNNWN--RFLNHGLEHLVQYRTDMDHSWT-----EOSVDYRHKFSLP 189
>B 245 VQENPQNFISRL-----FYEVVNSQTETHNVFYVQAEKCNPEFERNVENTSCFVVP 300
>Y 190 SYDGQKRYTFRVRSRNPIC-GSAQHWSEKSHPIHWG 225
>B 301 GVLPDTLNTVRIKVTNKLCEYDDKLWNSWQEMSIG 337

Search completed: March 3, 2004, 12:38:06
Job time : 39.9085 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 3, 2004, 12:24:04 ; Search time 55.3464 Seconds
(without alignments)
1184.377 Million cell updates/sec

Title: US-09-825-561A-4

Perfect score: 1288
Sequence: 1 LNTILPENGNETTADFFL.....QHWSESHPIHWSNTSKEN 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04.*

1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1288	100.0	232	5	AAE13727 Human sol
2	1288	100.0	341	7	ABR61610 IL-2 comm
3	1288	100.0	347	2	AAr47149 IL-2 rece
4	1288	100.0	357	7	ABR61609 IL-2 comm
5	1288	100.0	360	5	AAe13734 Human sol
6	1288	100.0	369	2	AAr47148 IL-2 rece
7	1288	100.0	369	5	AAU96932 Human cyt
8	1288	100.0	369	6	ABU03612 Human exp
9	1288	100.0	369	6	ABU03613 Human exp
10	1288	100.0	369	6	ABU03602 Human exp
11	1288	100.0	369	6	ABU03603 Human exp
12	1288	100.0	369	6	ABU03605 Human exp
13	1288	100.0	369	6	ABU03600 Human exp
14	1288	100.0	369	6	ABU03601 Human exp
15	1288	100.0	691	3	AAy92202 Fusion po
16	1288	100.0	691	6	ABU03610 Human exp
17	1288	100.0	694	3	AAy92201 Fusion po
18	1288	100.0	694	3	AAy92203 Fusion po
19	1288	100.0	694	6	ABU03611 Human exp
20	1288	100.0	694	6	ABU03609 Human exp
21	1282	99.5	482	2	AAW31646 Human cyt
22	1282	99.5	482	6	AAW31646 Human cyt
23	1277	99.1	230	2	AAr47151 IL-2 rece
24	1277	99.1	252	2	AAr47150 IL-2 rece
25	1277	99.1	252	6	ABU03606 Human exp

26	1272	98.8	230	2	ABR82934	AAr82934 Interleuk
27	960	74.5	363	4	ABr71882	ABr71882 Bos tauru
28	854.5	66.3	369	2	AAr59094	AAr59094 Murine IL
29	853.5	66.3	369	5	AAU77221	AAU77221 Mouse com
30	542	42.1	121	3	AAQ00283	AAQ00283 Human sec
31	542	42.1	121	6	ABU03604	ABU03604 Human exp
32	215	16.7	561	4	AAU69138	AAU69138 Canine IL
33	215	16.7	561	4	AAU69141	AAU69141 Canine IL
34	215	16.7	563	4	AAU69140	AAU69140 Canine IL
35	215	16.7	563	4	AAU69139	AAU69139 Canine IL
36	213	16.5	318	4	AAU69137	AAU69137 Canine IL
37	213	16.5	365	4	AAU69136	AAU69136 Canine in
38	213	16.5	386	4	AAU69135	AAU69135 Canine in
39	207	16.1	315	2	AAW56261	AAW56261 Mature in
40	207	16.1	317	5	AAE13746	AAE13746 Human sol
41	207	16.1	359	2	AAW56260	AAW56260 Construct
42	207	16.1	380	2	AAW36613	AAW36613 Human Zcy
43	207	16.1	380	2	AAW35295	AAW35295 Human IL-
44	207	16.1	380	2	AAW24972	AAW24972 Human int
45	207	16.1	380	2	AAW33603	AAW33603 Homo sapi

ALIGNMENTS

RESULT 1

AAE13727
ID AAE13727 standard; protein; 232 AA.

AC AAE13727;

XX
XX 26-FEB-2002 (first entry)

DE Human soluble IL-2Rgamma cytokine receptor protein fragment.

XX Human; Zalphall; cytokine receptor; immunosuppressive; cytostatic;
XX inflammatory disorder; haemostatic; cell proliferation; immune disorder;
XX autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
XX myaschonia gravis; systemic lupus erythematosus; SLE; diabetes; aschma;
XX ulcerative colitis; inflammatory bowel disease; Crohn's disease; sepsis;
XX viral infection; IL-2Rgamma.

OS Homo sapiens.

XX
XX WO200177171-A2.

PN
XX 18-OCT-2001.

PD
XX 03-APR-2001; 2001WO-US010872.

PF
XX 05-APR-2000; 2000US-0194731P.

PR
XX 28-JUL-2000; 2000US-0222121P.

PA (ZYMO) ZYMOGENETICS INC.

PI Sprechter CA, Novak JE, West JW, Presnell SR, Holly RD, Nelson AJ;

DR WPI; 2002-025898/03.

DR N-PSDB; AAD22319.

PT Novel soluble receptor polypeptides and polynucleotides used as cytokine
antagonist for stimulating ligand activity-induced proliferation of
hematopoietic cells and for suppressing immune response in a mammal.

PS Claim 29; Page 175-176; 243pp; English.

XX The invention relates to an isolated soluble zalphall cytokine receptor
polypeptide and their cDNA molecules. Zalpha proteins are useful for
inhibiting or antagonising the ligand activity-induced proliferation of
CC haematopoietic cells and haematopoietic cell progenitors preferably
CC lymphoid cells which are natural killer cells or cytotoxic T cells.
CC Zalphall is useful for treating immune and inflammatory disorders, for
reducing proliferation of neoplastic B or T cells, for suppressing an

CC immune response in a mammal exposed to an antigen or pathogen. Zalpha is
 CC useful for treating diseases that require immune regulation including
 CC autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,
 CC myasthenia gravis, systemic lupus erythematosus (SLE) and diabetes;
 CC asthma, ulcerative colitis, inflammatory bowel disease, Crohn's disease,
 CC sepsis, viral infection (dengue virus infection) and cancer. The present
 CC sequence is human soluble IL-2/gamma cytokine receptor cDNA fragment
 XX
 SQ Sequence 232 AA;

Query Match 100.0%; Score 1288; DB 5; Length 232;
 Best Local Similarity 100.0%; Pred. No. 3e-115;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTTILTPNGNEDTTADFFLTMTDLSVSTLPLPEVOCFVFNVEYMNCTWNSSEPO 60
 DB 1 LNTTILTPNGNEDTTADFFLTMTDLSVSTLPLPEVOCFVFNVEYMNCTWNSSEPO 60
 QY 61 TNLTLHWYKNSDNDKVKCQSHYLFSEETITSGCQLOKKEIHLYQTFVVOLODPREPRQA 120
 DB 61 TNLTLHWYKNSDNDKVKCQSHYLFSEETITSGCQLOKKEIHLYQTFVVOLODPREPRQA 120
 QY 121 TOMLKLQNLVWPAPENLTLLHKLSEQLNWNRRFLNCHLHLYQYRTDWDHSTEQSV 180
 DB 121 TOMLKLQNLVWPAPENLTLLHKLSEQLNWNRRFLNCHLHLYQYRTDWDHSTEQSV 180
 QY 181 DYRHKPSLPVDGQKRYTFRVRSRFPNPLCGSAQHWSEWSHPHIGSNTSKEN 232
 DB 181 DYRHKPSLPVDGQKRYTFRVRSRFPNPLCGSAQHWSEWSHPHIGSNTSKEN 232

RESULT 2
 ABR61610
 ID ABR61610 standard; peptide; 341 AA.
 XX
 AC ABR61610;
 DT 15-JAN-2004 (first entry)
 DE IL-2 common gamma chain (cgammac) fragment (residues 1-341).

XX IL-2; interleukin 2; common gamma chain; cgammac; antiinflammatory;
 KW gastrointestinal; antiarthritic; antirheumatic; osteopathic; cardiant;
 KW antisthmatic; noctropic; neuroprotective; antiarteriosclerotic;
 KW immunosuppressive; antithyroid; nuclear factor KB inducing kinase; NIK;
 KW gene therapy.

XX Homo sapiens.
 OS WO2003087374-A1.
 PN 23-OCT-2003.
 PD
 XX 15-APR-2003; 2003WO-IL000316.
 PF
 XX 18-APR-2002; 2002IL-00149217.
 PR 08-OCT-2002; 2002IL-00152183.
 XX
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 XX Wallach D, Ramakrishnan P, Shmushkovich T;
 PI WPI; 2003-845330/78.
 XX
 XX New interleukin-2 common gamma chain or its mutein, variant, fusion
 PT protein, functional derivative, circularly permuted derivative or
 PT fragment useful for treating Alzheimer's disease or atherosclerosis.
 XX
 XX Claim 6; Page 97-98; Opp; English.

PS The invention relates to an interleukin 2 (IL-2) common gamma chain
 CC (cgammac) or its mutein, variant, fusion protein, functional derivative,
 CC circularly permuted derivative or fragment. Specific antibodies and

CC small molecules capable of modulating the interaction between IL-2
 CC cgammac and nuclear factor KB inducing kinase (NIK) are useful for the
 CC manufacture of a medicament for the treatment of a disease, e.g. a
 CC disease resulting from excessive immune response such as rheumatoid
 CC arthritis, osteoarthritis, inflammatory bowel disease, asthma, cardiac
 CC infarct, Alzheimer's disease or atherosclerosis; or an autoimmune disease
 CC such as immune thyroiditis, or other arthropathies, e.g. autoimmune
 CC haemolytic anemia. The small molecule is useful for modulating signaling
 CC through cgammac. The present sequence represents an IL-2 cgammac protein
 CC fragment
 XX
 SQ Sequence 341 AA;

Query Match 100.0%; Score 1288; DB 7; Length 341;
 Best Local Similarity 100.0%; Pred. No. 5.2e-115;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTTILTPNGNEDTTADFFLTMTDLSVSTLPLPEVOCFVFNVEYMNCTWNSSEPO 60
 DB 23 LNTTILTPNGNEDTTADFFLTMTDLSVSTLPLPEVOCFVFNVEYMNCTWNSSEPO 82
 QY 61 TNLTLHWYKNSDNDKVKCQSHYLFSEETITSGCQLOKKEIHLYQTFVVOLODPREPRQA 120
 DB 83 TNLTLHWYKNSDNDKVKCQSHYLFSEETITSGCQLOKKEIHLYQTFVVOLODPREPRQA 142
 QY 121 TOMLKLQNLVWPAPENLTLLHKLSEQLNWNRRFLNCHLHLYQYRTDWDHSTEQSV 180
 DB 143 TOMLKLQNLVWPAPENLTLLHKLSEQLNWNRRFLNCHLHLYQYRTDWDHSTEQSV 202
 QY 181 DYRHKPSLPVDGQKRYTFRVRSRFPNPLCGSAQHWSEWSHPHIGSNTSKEN 232
 DB 203 DYRHKPSLPVDGQKRYTFRVRSRFPNPLCGSAQHWSEWSHPHIGSNTSKEN 254

RESULT 3
 AAR47149
 ID AAR47149 standard; protein; 347 AA.
 XX
 AC AAR47149;
 DT 25-MAR-2003 (revised)
 DT 13-JUN-1994 (first entry)
 DE IL-2 receptor gamma chain.
 XX
 KW Interleukin-2 receptor gamma chain; IL-2; receptor; immunoregulator;
 KW rheumatoid arthritis; transplant rejection; primer;
 KW polymerase chain reaction; PCR; amplification.

XX Homo sapiens.
 OS EP578932-A2.
 PN 19-JAN-1994.
 PD
 XX 22-APR-1993; 93EP-00106561.
 PF
 XX 23-APR-1992; 92JP-00104947.
 PR
 XX (AJIN) AJINOMOTO KK.
 PA (SUGA/) SUGAMURA K.
 XX
 XX Sugamura K, Takeshita T, Asao H, Nakamura M, Shimamura T;
 PI Suzuki M, Hamuro J;
 XX
 XX WPI; 1994-017546/03.
 DR N-FSDS; AAQ54829.
 XX
 XX DNA and protein sequences of IL-2 gamma chain - useful as immune
 PT regulatory agents for treatment of e.g. rheumatoid arthritis and
 PT transplant rejection.
 XX
 PS Claim 4; Page 41; 50pp; English.

XX The human IL-2 receptor gamma chain preform (AAR47148), including the
 CC signal peptide, is encoded by the sequence given in AAQ54828. The mature
 CC protein (AAR47149) is encoded by sequence AAQ54829. A soluble form of IL-
 CC 2 receptor gamma chain (AAR47150) is encoded by AAQ54830, while a soluble
 CC form suitable for expression in prokaryotes (AAR47151) is encoded by
 CC AAQ54831. Primers 1-6 (AAQ54820-25) are based on the N-terminal sequence
 CC of IL-2 receptor gamma chain, and are used to isolate IL2 receptor gamma
 CC chain receptor cDNA. Primers AAQ54826-27 are used to obtain the protein
 CC given in AAR47151. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 347 AA;

Query Match 100.0%; Score 1288; DB 2; Length 347;
 Best Local Similarity 100.0%; Pred. No. 5.3e-115;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVOCFVFNVEYMNCTWNSSEPOP 60
 DB 1 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVOCFVFNVEYMNCTWNSSEPOP 60
 QY 61 TNLTHWYKNSNDKVKQKSHYLFSEETSGCQKKEIHLVYQTFVVLQDPREPRQA 120
 DB 61 TNLTHWYKNSNDKVKQKSHYLFSEETSGCQKKEIHLVYQTFVVLQDPREPRQA 120
 QY 121 TOMLKLQNLVWPAPENLTLLHKLSEQLNWNRRFLNCHLEHLVQYRTDWDHSHWTEQSV 180
 DB 121 TOMLKLQNLVWPAPENLTLLHKLSEQLNWNRRFLNCHLEHLVQYRTDWDHSHWTEQSV 180
 QY 181 DYRHKPSLPSVDGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHMGNTSKEN 232
 DB 181 DYRHKPSLPSVDGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHMGNTSKEN 232

RESULT 4
 ABR61609
 ID ABR61609 standard; peptide; 357 AA.
 AC ABR61609;
 XX
 DT 15-JAN-2004 (first entry)
 DE IL-2 common gamma chain (cgammac) fragment (residues 1-357).
 XX

IL-2; interleukin 2; common gamma chain; cgammac; antiinflammatory;
 KW gastrointestinal; antiarthritic; antirheumatic; osteopathic; cardiant;
 KW antiasthmatic; nootropic; neuroprotective; antiarteriosclerotic;
 KW immunosuppressive; antithyroid; nuclear factor KB inducing kinase; NIK;
 KW gene therapy.

OS Homo sapiens.
 XX
 PN WO2003087374-A1.
 XX
 PD 23-OCT-2003.

XX 15-APR-2003; 2003WO-IL000316.

XX 18-APR-2002; 2002IL-00149217.

XX 08-OCT-2002; 2002IL-00152183.

XX (YEDA) YEDA RES & DEV CO LTD.

XX Wallach D, Ramakrishnan P, Shmushkovich T;

XX WPI; 2003-845330/78.

XX New interleukin-2 common gamma chain or its mutein, variant, fusion
 PT protein, functional derivative, circularly permuted derivative or
 PT fragment useful for treating Alzheimer's disease or atherosclerosis.

XX Claim 5; Page 96-97; Opp: English.

CC The invention relates to an interleukin 2 (IL-2) common gamma chain
 CC (cgammac) or its mutein, variant, fusion protein, functional derivative,
 CC circularly permuted derivative or fragment. Specific antibodies and
 CC small molecules capable of modulating the interaction between IL-2
 CC cgammac and nuclear factor KB inducing kinase (NIK) are useful for the
 CC manufacture of a medicament for the treatment of a disease, e.g. a
 CC disease resulting from excessive immune response such as rheumatoid
 CC arthritis, osteoarthritis, inflammatory bowel disease, asthma, cardiac
 CC infarct, Alzheimer's disease or atherosclerosis; or an autoimmune disease
 CC such as immune thyroiditis, or other arthropathies, e.g. autoimmune
 CC haemolytic anemia. The small molecule is useful for modulating signaling
 CC through cgammac. The present sequence represents an IL-2 cgammac protein
 CC fragment
 XX
 SQ Sequence 357 AA;

Query Match 100.0%; Score 1288; DB 7; Length 357;
 Best Local Similarity 100.0%; Pred. No. 5.5e-115;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVOCFVFNVEYMNCTWNSSEPOP 60
 DB 23 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVOCFVFNVEYMNCTWNSSEPOP 82
 QY 61 TNLTHWYKNSNDKVKQKSHYLFSEETSGCQKKEIHLVYQTFVVLQDPREPRQA 120
 DB 83 TNLTHWYKNSNDKVKQKSHYLFSEETSGCQKKEIHLVYQTFVVLQDPREPRQA 142
 QY 121 TOMLKLQNLVWPAPENLTLLHKLSEQLNWNRRFLNCHLEHLVQYRTDWDHSHWTEQSV 180
 DB 143 TOMLKLQNLVWPAPENLTLLHKLSEQLNWNRRFLNCHLEHLVQYRTDWDHSHWTEQSV 202
 QY 181 DYRHKPSLPSVDGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHMGNTSKEN 232
 DB 203 DYRHKPSLPSVDGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHMGNTSKEN 254

RESULT 5
 AAE13734
 ID AAE13734 standard; protein; 360 AA.
 AC AAE13734;
 XX
 DT 26-FEB-2002 (first entry)
 DE Human soluble IL-2gamma/kappa light chain chimeric DNA construct.

XX Human; Zalphall; cytokine receptor; immunosuppressive; cytostatic;
 KW inflammatory disorder; haemostatic; cell proliferation; immune disorder;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
 KW myasthenia gravis; systemic lupus erythematosus; SLE; diabetes; asthma;
 KW ulcerative colitis; inflammatory bowel disease; Crohn's disease; sepsis;
 KW viral infection; fusion protein; IL-2gamma.

OS Homo sapiens.

XX WO20017171-A2.

XX 18-OCT-2001.

XX 03-APR-2001; 2001WO-US010872.

XX 05-APR-2000; 2000US-0194731P.

XX 28-JUL-2000; 2000US-0222121P.

XX (ZYMO) ZYMOGENETICS INC.

XX Sprecher CA, Novak JB, West JW, Presnell SR, Holly RD, Nelson AJ;

XX WPI; 2002-025898/03.

XX N-PSDB; AAD22926.

XX Novel soluble receptor polypeptides and polynucleotides used as cytokine

PT antagonist for stimulating ligand activity-induced proliferation of
 XX hematopoietic cells and for suppressing immune response in a mammal.
 PS Example 28; Page 196-197; 243pp; English.
 XX The invention relates to an isolated soluble zalphal cytokine receptor
 CC polypeptide and their cDNA molecules. Zalpha proteins are useful for
 CC inhibiting or antagonising the ligand activity-induced proliferation of
 CC haematopoietic cells and haematopoietic cell progenitors preferably
 CC lymphoid cells which are natural killer cells or cytotoxic T cells.
 CC Zalpha is useful for treating immune and inflammatory disorders, for
 CC reducing proliferation of neoplastic B or T cells, for suppressing an
 CC immune response in a mammal exposed to an antigen or pathogen. Zalpha is
 CC useful for treating diseases that require immune regulation including
 CC autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,
 CC myasthenia gravis, systemic lupus erythematosus (SLE) and diabetes;
 CC asthma, ulcerative colitis, inflammatory bowel disease, Crohn's disease,
 CC sepsis, viral infection (dengue virus infection) and cancer. The present
 CC sequence is human soluble IL-2Rgamma/kappa light chain fusion protein
 CC construct
 XX Sequence 360 AA;
 SQ Query Match 100.0%; Score 1288; DB 5; Length 360;
 Best Local Similarity 100.0%; Pred. No. 5.6e-115;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPOP 60
 DB 23 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPOP 82
 QY 61 TNLTLHWYKNSDNDKVKQCSHYLFSEETSGCOLQKKEIHLIYQTFVVLQDPREPRQA 120
 DB 83 TNLTLHWYKNSDNDKVKQCSHYLFSEETSGCOLQKKEIHLIYQTFVVLQDPREPRQA 142
 QY 121 TQMLKLNLIWIPAPENLILHLKLSQLELNWNNRFLNHLVQYRTDWDHSTEQSV 180
 DB 143 TQMLKLNLIWIPAPENLILHLKLSQLELNWNNRFLNHLVQYRTDWDHSTEQSV 202
 QY 181 DYRKHSPLPSVDGQKRYTFRVSRFNPFCGSAQHSWSESHPIHWGNTSKEN 232
 DB 203 DYRKHSPLPSVDGQKRYTFRVSRFNPFCGSAQHSWSESHPIHWGNTSKEN 254
 RESULT 6
 ID AAR47148
 XX AAR47148 standard; protein; 369 AA.
 AC AAR47148;
 XX
 DT 25-MAR-2003 (revised)
 DT 13-JUN-1994 (first entry)
 XX
 XX IL-2 receptor gamma chain.
 XX Interleukin-2 receptor gamma chain; IL-2; receptor; immunoregulator;
 KW rheumatoid arthritis; transplant rejection; primer; PCR;
 KW polymerase chain reaction; amplification; ss.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FH Peptide 1..22
 FT /label= Sig_peptide
 FT
 XX EF578932-A2.
 XX
 XX 19-JAN-1994.
 XX
 XX 22-APR-1993; 93EP-00106561.
 XX
 XX 23-APR-1992; 92JP-00104947.
 XX

PA (AJIN) AJINOMOTO KK.
 XX (SUGA/) SUGAMURA K.
 PI Sugamura K, Takeshita T, Asao H, Nakamura M, Shimamura T;
 FI Suzuki M, Hamuro J;
 DR WPI; 1994-017546/03.
 DR N-PSDB; AAQ54828.
 XX DNA and protein sequences of IL-2 gamma chain - useful as immune
 PT regulatory agents for treatment of e.g. rheumatoid arthritis and
 PT transplant rejection.
 XX Disclosure; Page 16-17, 29-30; 50pp; English.
 XX The human IL-2 receptor gamma chain preform (AAR47148), including the
 CC signal peptide, is encoded by the sequence AAQ54828. The mature
 CC protein (AAR47149) is encoded by sequence AAQ54829. A soluble form of IL-
 CC 2 receptor gamma chain (AAR47150) is encoded by AAQ54830, while a soluble
 CC form suitable for expression in prokaryotes (AAR47151) is encoded by
 CC AAQ54831. Primers 1-6 (AAQ54820-25) are based on the N- terminal sequence
 CC of IL-2 receptor gamma chain, and are used to isolate IL2 receptor gamma
 CC chain receptor cDNA. Primers AAQ54826-27 are used to obtain the protein
 CC given in AAR47151. (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 369 AA;
 SQ Query Match 100.0%; Score 1288; DB 2; Length 369;
 Best Local Similarity 100.0%; Pred. No. 5.8e-115;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPOP 60
 DB 23 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPOP 82
 QY 61 TNLTLHWYKNSDNDKVKQCSHYLFSEETSGCOLQKKEIHLIYQTFVVLQDPREPRQA 120
 DB 83 TNLTLHWYKNSDNDKVKQCSHYLFSEETSGCOLQKKEIHLIYQTFVVLQDPREPRQA 142
 QY 121 TQMLKLNLIWIPAPENLILHLKLSQLELNWNNRFLNHLVQYRTDWDHSTEQSV 180
 DB 143 TQMLKLNLIWIPAPENLILHLKLSQLELNWNNRFLNHLVQYRTDWDHSTEQSV 202
 QY 181 DYRKHSPLPSVDGQKRYTFRVSRFNPFCGSAQHSWSESHPIHWGNTSKEN 232
 DB 203 DYRKHSPLPSVDGQKRYTFRVSRFNPFCGSAQHSWSESHPIHWGNTSKEN 254
 RESULT 7
 ID AAU96932
 XX AAU96932 standard; protein; 369 AA.
 AC AAU96932;
 XX
 DT 13-AUG-2002 (first entry)
 XX Human cytokine receptor common gamma chain.
 DE JAK3; cytostatic; immunomodulatory; antiinflammatory; graft rejection;
 KW human; antirheumatic; infection; hypogammaglobulinaemia; SCID;
 KW severe Combined immunodeficiency; Janus kinase; inflammation;
 KW rheumatoid arthritis; autoimmunity; gamma chain.
 XX Homo sapiens.
 XX US6372898-B1.
 XX
 XX 16-APR-2002.
 XX
 XX 13-NOV-1998; 98US-00191786.
 XX
 XX 13-NOV-1998; 98US-00191786.
 XX

PA (SCHE) SCHERING CORP.
 XX Cacalano NA, Johnston JA;
 XX WPI; 2002-433679/46.
 XX Jak3 variant polynucleotides useful for preventing, diagnosing and
 XX treating e.g. cancers, inflammation and rheumatoid arthritis.
 XX Example; Col 9-11; 25pp; English.
 XX This invention relates to a novel isolated human Jak3 variant
 XX polynucleotides. The Jak3 or gamma c polypeptides, mutants, fragments,
 XX and antibodies to them are useful for in vitro or in vivo screening or
 XX treatment of conditions associated with abnormal physiology or
 XX development, including abnormal proliferation, e.g. cancerous conditions,
 XX or degenerative conditions and severe infections due to reduced levels of
 XX T and natural killer (NK) cells, as well as hypogammaglobulinemia. The
 XX structural relationship of the Jak3 or gamma c protein to other Jak
 XX kinases suggests the possibility of biological activities beyond the
 XX Severe Combined Immunodeficiencies described patients with specific
 XX mutations in either the gamma c subunit of a cytokine receptor (e.g., IL-
 XX 2, IL-4, IL-7, IL-9, and IL-15) or in the Janus kinase. In particular,
 XX modulation of Jak kinase activities should be useful in situations where
 XX the Jak kinase functions have been implicated, e.g., lymphoid cell
 XX development, immunological responses, inflammation, graft rejection,
 XX rheumatoid arthritis, autoimmunity, abnormal proliferation, regeneration,
 XX degeneration, and atrophy of responsive cell types. For example, a
 XX disease or disorder associated with abnormal expression or abnormal
 XX signaling by Jak3 or gamma c protein (e.g., SCID, XSCID, inhibition of T
 XX cell proliferation, or similar phenotypes). The present sequence
 XX represents the human cytokine receptor common gamma chain protein
 XX sequence used to identify regions of JAK3 that are important for its
 XX interaction with the common gamma chain protein
 XX Sequence 369 AA;
 Query Match 100.0%; Score 1288; DB 5; Length 369;
 Best Local Similarity 100.0%; Pred. No. 5.8e-115;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 2y 1 LNTLTLPNGNEDTADFFLTMTDLSVSTLPLPEVQCFVFNVMCTWNSSEPP 60
 Db 23 LNTLTLPNGNEDTADFFLTMTDLSVSTLPLPEVQCFVFNVMCTWNSSEPP 82
 2y 61 TNLTLHYWYKNSDNDKVKQCSHYLFSEITSGCQLOKKEIHLVQTFVVLQDPRP 120
 Db 83 TNLTLHYWYKNSDNDKVKQCSHYLFSEITSGCQLOKKEIHLVQTFVVLQDPRP 142
 2y 121 TOMLKLQNLVFPAPENLTJLHKLSEQLNLNWNRFNLHCLVQYRTDWDHSTEQSV 180
 Db 143 TOMLKLQNLVFPAPENLTJLHKLSEQLNLNWNRFNLHCLVQYRTDWDHSTEQSV 202
 2y 181 DYRKHFSLPSVDGQKRYTFVRFRNPLCGSAQHSWSESHPIHWSNTSKEN 232
 Db 203 DYRKHFSLPSVDGQKRYTFVRFRNPLCGSAQHSWSESHPIHWSNTSKEN 254
 RESULT 8
 ID ABU03612
 XX ABU03612 standard; protein; 369 AA.
 XX AC ABU03612;
 XX 29-JAN-2003 (first entry)
 XX Human expressed protein tag (EPT) #278.
 XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 XX protease; protease inhibitor; transporter; cytoskeletal protein;
 XX receptor; transcription factor; cancer; MHC;
 XX major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.

XX Homo sapiens.
 XX WO200278524-A2.
 XX 10-OCT-2002.
 XX 28-MAR-2002; 2002WO-US009671.
 XX 28-MAR-2001; 2001US-0279495P.
 XX 21-MAY-2001; 2001US-0292544P.
 XX 08-AUG-2001; 2001US-0310801P.
 XX 01-OCT-2001; 2001US-0326370P.
 XX 04-DEC-2001; 2001US-0336780P.
 XX 20-FEB-2002; 2002US-0358985P.
 XX (ZYCO-) ZYCO INC.
 XX Chicz RM, Tomlinson AJ, Urban RG;
 WPI; 2003-040607/03.
 XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 XX cytoskeletal proteins, receptors or transcription factors), useful for
 XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 XX leukemia.
 XX Example 2; SEQ ID NO 278; 134pp; English.
 XX The invention describes a purified polypeptide, which comprises a
 XX fragment of a kinase, phosphatase, protease, protease inhibitor,
 XX transporter, cytoskeletal protein, receptor or transcription factor. The
 XX polypeptide is useful as an immunogenic composition for eliciting in a
 XX mammal an immunogenic response directed against any of the purified
 XX polypeptide. The purified polypeptide, or the antibody that binds to this
 XX polypeptide, is useful for treating cancer. The polypeptide is also
 XX useful for identifying compounds that binds to a naturally processed
 XX class I or class II MHC-binding polypeptide. The polypeptides and
 XX polynucleotides are particularly useful for treating or preventing
 XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 XX lymphoma or leukemia. These are also useful for screening agents for
 XX treating the above mentioned diseases. This sequence represents an
 XX expressed protein tag (EPT) isolated from human tissue for translational
 XX profiling. Note: This sequence does not appear in the printed
 XX specification but was obtained in electronic format directly from WIPO at
 XX ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 369 AA;
 Query Match 100.0%; Score 1288; DB 6; Length 369;
 Best Local Similarity 100.0%; Pred. No. 5.8e-115;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 2y 1 LNTLTLPNGNEDTADFFLTMTDLSVSTLPLPEVQCFVFNVMCTWNSSEPP 60
 Db 23 LNTLTLPNGNEDTADFFLTMTDLSVSTLPLPEVQCFVFNVMCTWNSSEPP 82
 2y 61 TNLTLHYWYKNSDNDKVKQCSHYLFSEITSGCQLOKKEIHLVQTFVVLQDPRP 120
 Db 83 TNLTLHYWYKNSDNDKVKQCSHYLFSEITSGCQLOKKEIHLVQTFVVLQDPRP 142
 2y 121 TOMLKLQNLVFPAPENLTJLHKLSEQLNLNWNRFNLHCLVQYRTDWDHSTEQSV 180
 Db 143 TOMLKLQNLVFPAPENLTJLHKLSEQLNLNWNRFNLHCLVQYRTDWDHSTEQSV 202
 2y 181 DYRKHFSLPSVDGQKRYTFVRFRNPLCGSAQHSWSESHPIHWSNTSKEN 232
 Db 203 DYRKHFSLPSVDGQKRYTFVRFRNPLCGSAQHSWSESHPIHWSNTSKEN 254
 RESULT 9
 ID ABU03613 standard; protein; 369 AA.

Query Match 100.0%; Score 1288; DB 6; Length 369;
 Best Local Similarity 100.0%; Pred. No. 5.8e-115;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTTLTPNGNEDTTADFLTTMTDLSVSTLPLPEVQCFVFNVMNCTWNSSEPPQ 60
 DB 23 LNTTLTPNGNEDTTADFLTTMTDLSVSTLPLPEVQCFVFNVMNCTWNSSEPPQ 82
 QY 61 TNLTHYWKNSDNDKVKQCSHYLFSEBITSGCOLQKKEIHLYQTFVVQLQDPREPRQA 120
 DB 83 TNLTHYWKNSDNDKVKQCSHYLFSEBITSGCOLQKKEIHLYQTFVVQLQDPREPRQA 142
 QY 121 TQMLKQLNLVWPAPENLTLLKLSQSQLELNNRFLNHCLEHLVQYRTDWDHSHWTQSV 180
 DB 143 TQMLKQLNLVWPAPENLTLLKLSQSQLELNNRFLNHCLEHLVQYRTDWDHSHWTQSV 202
 QY 181 DYRHKFSPLSDVGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHNGSNTSKEN 232
 DB 203 DYRHKFSPLSDVGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHNGSNTSKEN 254

RESULT 11
 ABU03603
 ID ABU03603 standard; protein; 369 AA.
 AC ABU03603;
 XX
 DT 29-JAN-2003 (first entry)
 DE Human expressed protein tag (EPT) #269.
 XX
 KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200278524-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 28-MAR-2002; 2002WO-US009671.
 XX
 PR 28-MAR-2001; 2001US-0279495P.
 PR 21-MAY-2001; 2001US-0292544P.
 PR 08-AUG-2001; 2001US-0310801P.
 PR 01-OCT-2001; 2001US-0326370P.
 PR 04-DEC-2001; 2001US-0336780P.
 PR 20-FEB-2002; 2002US-0358985P.
 XX
 PA (ZYCO-) ZYCOS INC.
 XX
 PI Chiciz RM, Tomlinson AJ, Urban RG;
 XX
 DR WPI; 2003-040607/03.
 XX
 PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.
 XX
 PS Example 2; SEQ ID NO 269; 134pp; English.

CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: this sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 369 AA;

Query Match 100.0%; Score 1288; DB 6; Length 369;
 Best Local Similarity 100.0%; Pred. No. 5.8e-115;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTTLTPNGNEDTTADFLTTMTDLSVSTLPLPEVQCFVFNVMNCTWNSSEPPQ 60
 DB 23 LNTTLTPNGNEDTTADFLTTMTDLSVSTLPLPEVQCFVFNVMNCTWNSSEPPQ 82
 QY 61 TNLTHYWKNSDNDKVKQCSHYLFSEBITSGCOLQKKEIHLYQTFVVQLQDPREPRQA 120
 DB 83 TNLTHYWKNSDNDKVKQCSHYLFSEBITSGCOLQKKEIHLYQTFVVQLQDPREPRQA 142
 QY 121 TQMLKQLNLVWPAPENLTLLKLSQSQLELNNRFLNHCLEHLVQYRTDWDHSHWTQSV 180
 DB 143 TQMLKQLNLVWPAPENLTLLKLSQSQLELNNRFLNHCLEHLVQYRTDWDHSHWTQSV 202
 QY 181 DYRHKFSPLSDVGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHNGSNTSKEN 232
 DB 203 DYRHKFSPLSDVGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHNGSNTSKEN 254

RESULT 12
 ABU03605
 ID ABU03605 standard; protein; 369 AA.
 XX ABU03605;
 XX
 DT 29-JAN-2003 (first entry)
 DE Human expressed protein tag (EPT) #271.
 XX
 KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200278524-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 28-MAR-2002; 2002WO-US009671.
 XX
 PR 28-MAR-2001; 2001US-0279495P.
 PR 21-MAY-2001; 2001US-0292544P.
 PR 08-AUG-2001; 2001US-0310801P.
 PR 01-OCT-2001; 2001US-0326370P.
 PR 04-DEC-2001; 2001US-0336780P.
 PR 20-FEB-2002; 2002US-0358985P.
 XX
 PA (ZYCO-) ZYCOS INC.
 XX
 PI Chiciz RM, Tomlinson AJ, Urban RG;
 XX
 DR WPI; 2003-040607/03.
 XX
 PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.

PT leukemia.
 PS Example 2; SEQ ID NO 271; 134pp; English.
 XX
 XX
 XX The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 369 AA;

Query Match 100.0%; Score 1288; DB 6; Length 369;
 Best Local Similarity 100.0%; Pred. No. 5.8e-115;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTTILTPNGNEDTTADFFLTMTPTDSLSVSTLPLPEVQCFFVFNVEYMNCTWNSSEPOP 60
 DB 23 LNTTILTPNGNEDTTADFFLTMTPTDSLSVSTLPLPEVQCFFVFNVEYMNCTWNSSEPOP 82
 QY 61 TNLTLHYWYKNSDNDKVKQKSHYLFSEETITSCQLQKKEIHLVQYTFVVLQDPREPRQA 120
 DB 83 TNLTLHYWYKNSDNDKVKQKSHYLFSEETITSCQLQKKEIHLVQYTFVVLQDPREPRQA 142
 QY 121 TQMLKQLNVLIPWAPENLTLHLKLSQLELNWNNRFLNHLCHLEHLVQYRTDWDHSTEQSV 180
 DB 143 TQMLKQLNVLIPWAPENLTLHLKLSQLELNWNNRFLNHLCHLEHLVQYRTDWDHSTEQSV 202
 QY 181 DYRHKFSLPVDGQKRYTFRVRSRFPNPLCGSAQHWSEWSHPHIGSNTSKEN 232
 DB 203 DYRHKFSLPVDGQKRYTFRVRSRFPNPLCGSAQHWSEWSHPHIGSNTSKEN 254

RESULT 13
 ABU03600
 ID ABU03600 standard; protein; 369 AA.
 XX
 XX ABU03600;
 XX
 XX 29-JAN-2003 (first entry)
 XX Human expressed protein tag (EPT) #266.
 XX
 XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
 XX
 XX Homo sapiens.
 XX
 XX W0200278524-A2.
 XX
 XX 10-OCT-2002.
 XX
 XX 28-MAR-2002; 2002WO-US009671.
 XX
 XX 28-MAR-2001; 2001US-0279495P.
 XX 21-MAY-2001; 2001US-0292544P.
 XX 08-AUG-2001; 2001US-0310801P.
 XX 01-OCT-2001; 2001US-0326370P.

PR 04-DEC-2001; 2001US-0336780P.
 PR 20-FEB-2002; 2002US-0358985P.
 XX
 XX (ZYCO-) ZYCOS INC.
 XX
 XX Chicz RM, Tomlinson AJ, Urban RG;
 XX
 XX WPI; 2003-040607/03.
 XX
 XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.

Example 2; SEQ ID NO 266; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

Sequence 369 AA;

Query Match 100.0%; Score 1288; DB 6; Length 369;
 Best Local Similarity 100.0%; Pred. No. 5.8e-115;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTTILTPNGNEDTTADFFLTMTPTDSLSVSTLPLPEVQCFFVFNVEYMNCTWNSSEPOP 60
 DB 23 LNTTILTPNGNEDTTADFFLTMTPTDSLSVSTLPLPEVQCFFVFNVEYMNCTWNSSEPOP 82
 QY 61 TNLTLHYWYKNSDNDKVKQKSHYLFSEETITSCQLQKKEIHLVQYTFVVLQDPREPRQA 120
 DB 83 TNLTLHYWYKNSDNDKVKQKSHYLFSEETITSCQLQKKEIHLVQYTFVVLQDPREPRQA 142
 QY 121 TQMLKQLNVLIPWAPENLTLHLKLSQLELNWNNRFLNHLCHLEHLVQYRTDWDHSTEQSV 180
 DB 143 TQMLKQLNVLIPWAPENLTLHLKLSQLELNWNNRFLNHLCHLEHLVQYRTDWDHSTEQSV 202
 QY 181 DYRHKFSLPVDGQKRYTFRVRSRFPNPLCGSAQHWSEWSHPHIGSNTSKEN 232
 DB 203 DYRHKFSLPVDGQKRYTFRVRSRFPNPLCGSAQHWSEWSHPHIGSNTSKEN 254

RESULT 14
 ABU03601
 ID ABU03601 standard; protein; 369 AA.
 XX
 XX ABU03601;
 XX
 XX 29-JAN-2003 (first entry)
 XX Human expressed protein tag (EPT) #267.
 XX
 XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
 XX

OS Homo sapiens.
FN WO200278524-A2.
PD 10-OCT-2002.
XX 28-MAR-2002; 2002WO-US009671.
XX 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX (ZYCO-) ZYCO INC.
FA Chicz RM, Tomlinson AJ, Urban RG;
FI WPI; 2003-040607/03.
DR New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
PT Example 2; SEQ ID NO 267; 134pp; English.
PS The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, or protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 369 AA;
SQ
Query Match 100.0%; Score 1288; DB 6; Length 369;
Best Local Similarity 100.0%; Pred. No. 5.8e-115; Indels 0; Gaps 0;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNTLITLTPNGNEDTTADFFLTMTPTDSLVSSTLPLPEVQCFVFNVEYMNCTWNSSESPQP 60
Db 23 LNTLITLTPNGNEDTTADFFLTMTPTDSLVSSTLPLPEVQCFVFNVEYMNCTWNSSESPQP 82
QY 61 TNLTLHYWYKNSDNDKVKQCSHYLFSEBITSGCQLOKKEIHLVYTFVQLODPRPRQA 120
Db 83 TNLTLHYWYKNSDNDKVKQCSHYLFSEBITSGCQLOKKEIHLVYTFVQLODPRPRQA 142
QY 121 TQMLKQLNLVLPWAPENLTMLKLSQLELNWNRFLNHLVQVYRTDWDHSWTQSV 180
Db 143 TQMLKQLNLVLPWAPENLTMLKLSQLELNWNRFLNHLVQVYRTDWDHSWTQSV 202
QY 181 DYRHKFSLPSVDGQKRYFRVRSFNPFLCGSAQHSWSHPHIGWNTSKEN 232
Db 203 DYRHKFSLPSVDGQKRYFRVRSFNPFLCGSAQHSWSHPHIGWNTSKEN 254
RESULT 15
AA92202
ID AAY92202 standard; protein; 691 AA.
XX

AC AAY92202;
XX 01-AUG-2000 (first entry)
XX Fusion polypeptide 603, IL-4 trap.
XX IL-4 trap; cytokine; antagonist; CNTF; receptor; fusion protein;
XX cytostatic; immunomodulator; osteopathic.
XX Synthetic.
XX Homo sapiens.
XX WO200018932-A2.
XX 06-APR-2000.
XX 22-SEP-1999; 99WO-US022045.
XX 25-SEP-1998; 98US-0101858P.
XX 19-MAY-1999; 99US-00313942.
XX (REGS-) REGENERON PHARM INC.
XX Stahl N, Yancopoulos GD;
XX WPI; 2000-293165/25.
XX N-PSDB; AAA09044.
XX Isolated nucleic acid molecule for treating cytokine-related diseases or
XX disorders encodes a fusion polypeptide capable of binding a cytokine to
XX form a nonfunctional complex.
XX Example 6; Fig 22A-D; 152pp; English.
XX This sequence shows fusion polypeptide 603, which is capable of binding
XX cytokine IL-4 to form a non-functional complex. The invention concerns
XX production of antagonists to any cytokine that utilizes an alpha
XX specificity determining component, which when combined with the cytokine,
XX binds to a first beta signal transducing component to form a non-
XX functional intermediate which then binds to a second beta signal
XX transducing component causing beta-receptor dimerization, the soluble
XX alpha specificity determining component of the receptor (SR-alpha) and
XX of the extracellular domain of the first beta signal transducing component
XX of the cytokine receptor (beta-1) are combined to form heterodimers (SR-
XX alpha:beta-1) that act as antagonist to the cytokine by binding the
XX cytokine to form a non-functional complex. The receptor components are
XX shared by cytokines such as the CNTF (Ciliary neurotrophic factor) family
XX of cytokines. The invention provides the basis for the development of IL-
XX 6 antagonists, as they show that if, in the presence of a ligand, a non-
XX functional intermediate complex, consisting of the ligand, its alpha
XX receptor and its beta-1 receptor component, can be formed, it will
XX effectively block the action of the ligand. Effective antagonists of IL-6
XX or CNTF consist of heterodimers of the extracellular domains of the alpha
XX specificity determining components of their receptors and the
XX extracellular domain of gp130. The resultant heterodimers, function as
XX high-affinity traps, rendering the cytokine inaccessible to form a signal
XX transducing complex with the native membrane-bound forms of their
XX receptor. The nucleic acids and polypeptides are useful for treating
XX cytokine-related diseases or disorders such as osteoporosis and primary
XX and secondary effects of cancer including multiple myeloma or cachexia
XX Sequence 691 AA;
SQ
Query Match 100.0%; Score 1288; DB 3; Length 691;
Best Local Similarity 100.0%; Pred. No. 1.4e-114; Indels 0; Gaps 0;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNTLITLTPNGNEDTTADFFLTMTPTDSLVSSTLPLPEVQCFVFNVEYMNCTWNSSESPQP 60
Db 23 LNTLITLTPNGNEDTTADFFLTMTPTDSLVSSTLPLPEVQCFVFNVEYMNCTWNSSESPQP 82
QY 61 TNLTLHYWYKNSDNDKVKQCSHYLFSEBITSGCQLOKKEIHLVYTFVQLODPRPRQA 120
XX

Db	83	TNLTLYWYKNSDNDKVKCSHYLFSEBITSCCQLQKKEIHLVQTFVVQLQDPREPRQA	142
Qy	121	TOMLKLONLVIFWAPENLTLHKLSQSLELNWNNRFLNHCLEHLVQYRTDWDHSHWTQSV	180
Db	143	TOMLKLONLVIFWAPENLTLHKLSQSLELNWNNRFLNHCLEHLVQYRTDWDHSHWTQSV	202
Qy	181	DYRHKFSLPSVDGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHMGNTSKEN	232
Db	203	DYRHKFSLPSVDGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHMGNTSKEN	254

Search completed: March 3, 2004, 12:35:37
Job time : 57.3464 secs

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DM protein - protein search, using sw model

Run on: March 3, 2004, 12:31:14 ; Search time 26.4706 Seconds
(without alignments)
1930.971 Million cell updates/sec

Title: US-09-825-561A-10

Perfect score: 850

Sequence: 1 MRSSPGNMERIVCLMVFL.....LLQKMIHQLSRTHGSEDS 162

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 31518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	850	100.0	162	4 Q9HBE4	Q9HBE4 homo sapien
2	486	57.2	146	11 Q9ES17	Q9ES17 mus musculus
3	392	46.1	123	11 Q80XG2	Q80XG2 peromyscus
4	85	10.0	311	5 Q81913	Q81913 loxosceles
5	84.5	9.9	722	16 Q8D8P4	Q8D8P4 vibrio vuln
6	83.5	9.8	582	16 Q8DJS6	Q8DJS6 synchococc
7	83.5	9.8	3052	12 Q82933	Q82933 johnsongras
8	83	9.8	899	2 Q82336	Q82336 salmorella
9	83	9.8	899	2 Q822J7	Q822J7 shigella so
10	83	9.8	1224	16 Q8CPT9	Q8CPT9 staphylococ
11	81.5	9.6	566	5 Q8VY88	Q8VY88 drosophila
12	81	9.5	140	13 Q8JFF4	Q8JFF4 anas platyr
13	81	9.5	163	5 Q966R0	Q966R0 dictyosteli
14	81	9.5	385	5 Q9VJL7	Q9VJL7 drosophila
15	81	9.5	414	5 Q9NK60	Q9NK60 drosophila
16	80	9.4	140	13 Q804B7	Q804B7 cairina mos

Q8ik96 plasmodium
Q9w756 gallus gall
Q91y09 mus musculu
Q80x92 mus musculu
Q8euw0 mycoplasma
Q8mua4 drosophila
Q9jj48 mus musculu
Q7xvp8 oryza sativ
Q9ell4 homo sapien
Q8wvp0 homo sapien
Q8myv8 drosophila
Q9vy89 drosophila
Q23239 calliphora
Q9w3h8 drosophila
Q8wrs2 drosophila
Q8wrs3 drosophila
Q9w3hc drosophila
Q8erw4 encephalito
Q86iv0 dictyosteli
Q9dev5 gallus gall
Q9bfc3 didelphis m
Q22975 caenorhabdi
Q8k5l8 streptococc
Q8blai mus musculu
Q86k11 dictyosteli
Q8lrp4 drosophila
Q8i3m4 plasmodium
Q8iil9 plasmodium
Q9ec15 homo sapien

ALIGNMENTS

RESULT 1

Q9HBE4
ID Q9HBE4 PRELIMINARY; PRT; 162 AA.
AC Q9HBE4;
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Interleukin 21.
GN IL21.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20331754; PubMed=11081504;
RA Parrish-Novak J., Dillon S.R., Nelson A., Hammond A., Sprecher C.,
RA Gross J.A., Johnston J., Madden K., Xu W., West J., Schrader S.,
RA Burkhead S., Heipel M., Brandt C., Kuipjer J.L., Kramer J.,
RA Conklin D., Presnell S.R., Berry J., Shiota F., Bort S., Hamby K.,
RA Mudri S., Clegg C., Moore M., Grant F.J., Lofton-Day C., Gilbert T.,
RA Rayond F., Ching A., Yao L., Smith D., Webster P., Whitmore T.,
RA Maurer M., Kaushansky K., Holly R.D., Foster D.;
RT "Interleukin 21 and its receptor are involved in NK cell expansion and
regulation of lymphocyte function.";
RL Nature 408:57-63(2000).
EMBL; AF254069; AAG29348.1; ..
DR Genew; HGNC:6005; IL21.
DR GO; GO:0005634; Cnucleus; NAS
DR GO; GO:0005125; Fcytokine activity; NAS.
DR GO; GO:0007515; P.lymph gland development; NAS.
DR GO; GO:0007165; P.signal transduction; NAS.
SQ SEQUENCE 162 AA; 18652 MW; 54EFD4ED3AB97FE CRC64;

Query Match 100.0%; Score 850; DB 4; Length 162;

Best Local Similarity 100.0%; Pred. No. 8.7e-80;

Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSPGNMERIVCLMVFLGTLVHKSSSQGDHMRQLDIVDLQKNVNDLVEEF 60

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Db 1 MRSSPGNMRIVICLVIFLGTIVLHKSSSQGDREIMRQLDIVDQLKNYVNDLVPEP 60
Qy 61 LPAPEDVETNCWAFSCFOKQALKSANTGNNEIINVSIKLKRKPPSTNAGRRQKRL 120
Db 61 LPAPEDVETNCWAFSCFOKQALKSANTGNNEIINVSIKLKRKPPSTNAGRRQKRL 120
Qy 121 TCPSCDSYKPKPPKFFLRPFKSLQKMIHQHLSRTHGSEDS 162
Db 121 TCPSCDSYKPKPPKFFLRPFKSLQKMIHQHLSRTHGSEDS 162
RESULT 2
Q9ES17 PRELIMINARY; PRT; 146 AA.
AC Q9ES17;
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Interleukin 21.
GN IL21.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BAUB/C;
RX MEDLINE=20531754; PubMed=11081504;
RA Parrish-Novak J., Dillon S.R., Nelson A., Hammond A., Sprecher C.,
RA Gross J.A., Johnston J., Madden K., Xu W., West J., Schrader S.,
RA Burkhead S., Heibel M., Brandt C., Kuljper J.L., Kramer J.,
RA Conklin D., Presnell S.R., Berry J., Shiota F., Bort S., Hamby K.,
RA Mudri S., Clegg C., Moore M., Grant F.J., Lofton-Day C., Gilbert T.,
RA Raymond F., Chang A., Yao L., Smith D., Webster P., Whitmore T.,
RA Maurer M., Kaushansky K., Holly R.D., Foster D.;
RA "Interleukin 21 and its receptor are involved in NK cell expansion and
RT regulation of lymphocyte function.";
RL Nature 408:57-63(2000).
DR EMBL; AF254070; AAG29349.1; -.
DR MGD; MGI:1890474; IL21.
DR GO; GO:0005126; Phenatopoietin/interferon-class (D200-domain. .; IDA.
SQ SEQUENCE 146 AA; 16811 MW; D2527ED958A15194 CRC64;

Query Match 57.2%; Score 486; DB 11; Length 146;
Best Local Similarity 63.0%; Pred. No. 2.9e-42;
Matches 92; Conservative 23; Mismatches 31; Indels 0; Gaps 0;

Qy 8 MERIVICLVIFLGTIVLHKSSSQGDREIMRQLDIVDQLKNYVNDLVPELPAPEDV 67
Db 1 MERTVLCVIFLGTIVLHKSSSQGDREIMRQLDIVDQLKNYVNDLVPELPAPEDV 60
Qy 68 ETNCWAFSCFOKQALKSANTGNNEIINVSIKLKRKPPSTNAGRRQKRLTCPSCDS 127
Db 61 KGHCHEAFACTQKAKLKFSGNKNKTFIDLVQALRRRLPARRGKKQKHLAKPCSDS 120
Qy 128 YKPKPKFFLRPFKSLQKMIHQHLS 153
Db 121 YKRTPKFFLRKSLQKMIHQHLS 146

RESULT 3
Q80XG2 PRELIMINARY; PRT; 123 AA.
AC Q80XG2;
DT 01-JUN-2003 (TREMELrel. 24, Created)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Interleukin-21 (Fragment).
GN IL21.
OS Peromyscus maniculatus (Deer mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;

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OC Peromyscus.
OX NCBI_TaxID=10042;
RN [1]
RP SEQUENCE FROM N.A.
RA Scheut T., Buniger A., Davenport B., Hegg T.;
RT "Cloning of deer mouse IL-2, IL-12 p35, IL-21, GM-CSF, CCL3 and CCL4
RT CDNA's.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY247761; AAP04420.1; -.
FT NON_TER 1
FT NON_TER 123
SQ SEQUENCE 123 AA; 13945 MW; 8656C8EA95447E34 CRC64;

Query Match 46.1%; Score 392; DB 11; Length 123;
Best Local Similarity 60.2%; Pred. No. 1.2e-32;
Matches 74; Conservative 24; Mismatches 25; Indels 0; Gaps 0;

Qy 16 MVIFLGTIVLHKSSSQGDREIMRQLDIVDQLKNYVNDLVPELPAPEDVETNCWESA 75
Db 1 VVIFLGTIVLHKSSSQGDREIMRQLDIVDQLKNYVNDLVPELPAPEDVETNCWESA 60
Qy 76 FSCFOKQALKSANTGNNEIINVSIKLKRKPPSTNAGRRQKRLTCPSCDSYKPKPKPE 135
Db 61 FACFOKALKPANTGSKNTIISDLVTQLRRRLPATKAEKQKQSLVKPCDSYKPKPKPE 120
Qy 136 FLE 138
Db 121 FLE 123

RESULT 4
Q81913 PRELIMINARY; PRT; 311 AA.
ID Q81913
AC Q81913;
DT 01-MAR-2003 (TREMELrel. 23, Created)
DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Sphingomyelinase-like protein.
OS Loxosceles laeta.
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Haplogynae; Sicariidae; Loxosceles.
OX NCBI_TaxID=58217;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX MEDLINE=22306580; PubMed=12419302;
RA Pedrosa M.F.F., Junqueira de Azevedo I.L.M.,
RA Goncalves-de-Andrade R.M., van den Berg C.W., Ramos C.R.R., Ho P.L.,
RA Tambourgi D.V.;
RA "Molecular cloning and expression of a functional dermonecrotic and
RT haemolytic factor from Loxosceles laeta venom.";
RL Biochem. Biophys. Res. Commun. 298:638-645(2002).
DR EMBL; AY093600; AAM21155.1; -.
DR GO; GO:0008889; F:glycerophosphodiester phosphodiesterase act. .; IEA.
DR GO; GO:0006071; P:glycerol metabolism; IEA.
DR InterPro; IPR004129; GDPD.
DR Pfam; PF03009; GDPD; 1.
SQ SEQUENCE 311 AA; 35451 MW; 39040BB3A21F56E1 CRC64;

Query Match 10.0%; Score 85; DB 5; Length 311;
Best Local Similarity 23.1%; Pred. No. 1.8;
Matches 42; Conservative 23; Mismatches 71; Indels 46; Gaps 7;

Qy 11 IVICLVIFLGTIVLHKSSSQGDREIMRQLDIVDQLKNYVNDLVPELPAPEDV 57
Db 8 ILGCVTILGQATDVGERADKERPIWNLGHMVNAVKQPTFLNDGANAIEADITPKGAV 67
Qy 58 P--EFLPAPEDVETNC--EWSAFSCFOKA-----OLKSANTGNNE 93
Db 68 PTYSYHGTPCDFGRDCIRWEYFDVFLQTLRDYTPGNSKYKFKFILFVLDLTKGSNNNE 127
Qy 94 -RIINYSIKK--LKRKPPSTNAGRRQKRLTCPSCDSYKPKPKPELFKSLQKMIHQ 150

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Db 128 VRAGENIAKGLLNKYNWNGNGRAYVLSLDIAHY-----EFIRPKFVLKAEH 181

2y 151 HL 152

2b 182 NL 183

RESULT 5

28D6P4 PRELIMINARY; PRT; 722 AA.

AC Q8D6P4; 23, Created)

DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)

DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)

DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)

DE ABC-type bacteriocin/antibiotic exporters.

3N VV20484.

3S Vibrio vulnificus.

3C Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;

3C Vibrionaceae; Vibrio.

3X NCBI_TaxID=672;

3N [1]

3P SEQUENCE FROM N.A.

3C STRAIN=CMCP6;

3A Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,

3A Choy H.E.;

3T "Complete genome sequence of *Vibrio vulnificus* CMCP6.";

3L Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.

3R EMBL; AB016809; AAC07435.1; -

3R GO; GO:0016020; C:membrane; IEA.

3R GO; GO:0005524; F:ATP binding; IEA.

3R GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. .; IEA.

3R GO; GO:0000166; F:nucleotide binding; IEA.

3R GO; GO:0004849; F:uridine kinase activity; IEA.

3R GO; GO:0006810; P:transport; IEA.

3R InterPro; IPR003593; AAA_ATPase.

3R InterPro; IPR001140; ABC_TM_transport.

3R InterPro; IPR003439; ABC_transporter.

3R InterPro; IPR000764; Uridine kin.

3R Pfam; PF00664; ABC membrane; 1.

3R Pfam; PF00005; ABC tran; 1.

3R PRINTS; PR00988; URIDINKINASE.

3R PRODOM; PD000006; ABC transporter; 1.

3R SMART; SM00382; AAA_1.

3R PROSITE; PS00211; ABC_TRANSPORTER_1; 1.

3R PROSITE; PS00893; ABC_TRANSPORTER_2; 1.

3R Complete proteome.

3Q SEQUENCE 722 AA; 79857 MW; B8967F3B930C0205 CRC64;

Query Match 9.8%; Score 84.5; DB 16; Length 722;

Best Local Similarity 25.0%; Pred. No. 5.4;

Matches 36; Conservative 26; Mismatches 57; Indels 25; Gaps 6;

Qy 17 VIFGLTLVHKSSSQGDHRMI-----RMRQLDIVDQLKYNVDL---VPEFLPA 63

Db 32 VVYAGQPHKKSSSQQLKHALGVSHLSDMEMREADYLG-LKSQVTLTQALDTLPL 90

Qy 64 PEDVETNCWAFSCFQXQALKSANTGNNEIRINVISIKLKKPKPSTNAGRQKRLTCTP 123

Db 91 PALIENNHGW-----QVITQVSDGHWTFFDPSTQQLQTPVSENPQR-KHKVMLL 140

Qy 124 SCDSYEKKPKPEFLERF-KSLQK 146

Db 141 ADEQLSSKEVKFGLSWFAPSILRQ 164

RESULT 6

Q8DJS6 PRELIMINARY; PRT; 582 AA.

AC Q8DJS6; 23, Created)

DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)

DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)

DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)

DE Tlr1146 protein.

GN TLR1146.

OS Synecococcus elongatus (Thermosynechococcus elongatus).

OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.

OX NCBI_TaxID=32046;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BP-1;

RX MEDLINE=2225144; PubMed=12240834;

RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,

RA Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,

RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,

RA Shimpou S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;

RT "Complete genome structure of the thermophilic cyanobacterium

RT Thermosynechococcus elongatus BP-1.";

RL DNA Res. 9,123-130(2002).

RL EMBL; AF005372; BAC08698.1; -

DR GO; GO:0016020; C:membrane; IEA.

DR InterPro; IPR006685; MSion_channel.

DR Pfam; PF00924; MS_channel; 1.

KW Complete proteome.

3Q SEQUENCE 582 AA; 66407 MW; DFOA33E93614A92D CRC64;

Query Match 9.8%; Score 83.5; DB 16; Length 582;

Best Local Similarity 21.6%; Pred. No. 5.4;

Matches 21; Conservative 24; Mismatches 31; Indels 21; Gaps 3;

Qy 81 KAQLKSANTGNNEIRINVISIKLKKPKPSTNAGRQKHER-----LTCP 123

Db 91 RAELIQSNL---RAVLHSALEADRRSPARVDIGVARLHNLVISARIGQABRTTLLT 147

Qy 124 SCDS-YEKKPKPEFLERF-KSLQKHLSSRTGHS 159

Db 148 EADSDYHQLPPETLAQQRDILQEQMNAIQERTHAA 184

RESULT 7

Q82933 PRELIMINARY; PRT; 3052 AA.

AC Q82933; 01, Created)

DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)

DT 01-JAN-1998 (TREMELrel. 05, Last annotation update)

DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)

DE Viral proteins.

OS Johnsongrass mosaic virus.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;

OC Potyvirus.

OX NCBI_TaxID=31742;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=94200956; PubMed=8150599;

RA Gough K.H., Shukla D.D.;

RT "the nucleotide sequence of Johnson grass mosaic potyvirus genomic

RT RNA.";

RL Intervirology 36:181-192(1993).

RL [2]

RP SEQUENCE FROM N.A.

RA Gough K.H.;

RL Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.

RL [3]

RP SEQUENCE FROM N.A.

RA Nurhayati E.;

RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.

DR EMBL; Z36920; CAAB1549.1; -

DR MEROPS; C04_011; -

DR MEROPS; C06_001; -

DR MEROPS; S30_001; -

DR GO; GO:0019028; C:viral capsid; IEA.

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0008026; F:ATP dependent helicase activity; IEA.

DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.

DR GO; GO:0016787; F:hydrolase activity; IEA.

DR GO; GO:0003676; F:nucleic acid binding; IEA.

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DR GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO:0006128; F:structural molecule activity; IEA.
DR GO:0006508; F:proteolysis and peptidolysis; IEA.
DR GO:0006350; F:transcription; IEA.
DR GO:0009079; F:viral genome replication; IEA.
DR InterPro: IPR001410; DEAD.
DR InterPro: IPR001650; Helicase C.
DR InterPro: IPR001730; Peptidase C4.
DR InterPro: IPR001456; Peptidase C6.
DR InterPro: IPR001592; Pcty-coat.
DR InterPro: IPR002540; Pcty-Fi.
DR InterPro: IPR007095; RNA_pol_DS_PS.
DR InterPro: IPR001205; RNA_pol_P3D.
DR InterPro: IPR001205; RNA_pol_P3D.
DR InterPro: IPR007094; RNA_pol_P5vir.
DR Pfam: PF00271; helicase C; 1.
DR Pfam: PF00863; Peptidase C4; 1.
DR Pfam: PF00851; Peptidase C6; 1.
DR Pfam: PF00767; Pcty-coat; 1.
DR Pfam: PF01577; Pcty-Fi; 1.
DR Pfam: PF00680; RNA_Dep_RNA_pol; 1.
DR PRINTS: PRO0966; NIAPCTPTASE.
DR SMART: SM00487; DEXDC; 1.
DR SMART: SM00490; HELIC; 1.
KW ATP-binding; Coat protein; Helicase; Hydrolase.
FT CHAIN 239 699 HELPER COMPONENT (HC).
FT CHAIN 700 1046 PROTEASE3.
FT CHAIN 1047 1098 6K1.
FT CHAIN 1099 1757 CYTOPLASMIC INCLUSION (CI).
FT CHAIN 1758 1803 6K2.
FT CHAIN 1804 1991 SMALL NUCLEAR INCLUSION/VIRUS ATTACHED
FT CHAIN 1992 2233 PROTEIN.
FT CHAIN 2234 2749 SMALL NUCLEAR INCLUSION/PROTEASE.
FT CHAIN 2750 3052 LARGE NUCLEAR INCLUSION/POLYMERASE.
FT CHAIN 3052 AA; 347247 MW; 08CD8831A73EBCA9 CRC64;
SQ SEQUENCE 3052 AA; 347247 MW; 08CD8831A73EBCA9 CRC64;

Query Match 9.8%; Score 83.5; DB 12; Length 3052;
Best Local Similarity 23.1%; Pred. No. 38;
Matches 25; Conservative 23; Mismatches 57; Indels 3; Gaps 3;

QY 45 IVDLQNYNDLVPRFLPAPEDVETNCVSAFCFOAKLKSANTGNRIINVISIKLK 104
Db 220 LVNALDQYED-VKQICHYSFDAARAFKGTENTHTAQRREAHDTNHEPV-MSVEBCG 277
QY 105 RKPPSTNAGROKRLHLCQSC-DSYKPKPKFLERFKSLLOKWLHIOH 151
Db 278 RRAAMLENAPHQGFKTKCKCFQTFDEHSDDEVCEIHNALQRIEQN 325

RESULT 8
ID Q52336 PRELIMINARY; PRT; 899 AA.
AC Q52336;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE NIKB protein.
GN NIKB.
OS Salmonella typhimurium.
OC Plasmid R64.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=drd-11; PLASMID=R64;
RX MEDLINE=96198148; PubMed=8626273;
RA Furuya N., Komano T.;
RT "Nucleotide sequence and characterization of the trbABC region of the IncII plasmid R64: existence of the pnd gene for plasmid maintenance within the transfer region.";
RT J. Bacteriol. 178:1491-1497(1996).
RN [2]

SEQUENCE FROM N.A.
RC STRAIN=drd-11; PLASMID=R64;
RX MEDLINE=92011438; PubMed=1917882;
RA Furuya N., Komano T.;
RT "Determination of the nick site at orit of IncII plasmid R64: global similarity of orit structures of IncII and INCP plasmids.";
RT J. Bacteriol. 173:6612-6617(1991).
RN [5]
SEQUENCE FROM N.A.
RC STRAIN=drd-11; PLASMID=R64;
RX MEDLINE=98053841; PubMed=9393692;
RA Furuya N., Komano T.;
RT "Mutational analysis of the R64 orit region: requirement for precise location of the Nika-binding sequence.";
RT J. Bacteriol. 179:7291-7297(1997).
RN [6]
SEQUENCE FROM N.A.
RC STRAIN=drd-11; PLASMID=R64;
RX MEDLINE=98268996; PubMed=9603870;
RA Yoshida T., Furuya N., Ishikura M., Isobe T., Haino-Fukushima K., Ogawa T., Komano T.;
RT "Purification and characterization of thin pili of IncII plasmids Colib-P9 and R64: formation of Pili-specific cell aggregates by type IV pili.";
RT J. Bacteriol. 180:2842-2848(1998).
RN [7]
SEQUENCE FROM N.A.
RC STRAIN=drd-11; PLASMID=R64;
RX MEDLINE=94132048; PubMed=8300611;
RA Pansegrau W., Schroder W., Lanka E.;
RT "Concerted action of three distinct domains in the DNA cleaving-joining reaction catalyzed by relaxase (TraI) of conjugative plasmid RP4.";
RT J. Biol. Chem. 269:2782-2789(1994).
RN [8]
SEQUENCE FROM N.A.
RC STRAIN=drd-11; PLASMID=R64;
RX MEDLINE=94285211; PubMed=8014987;
RA Pansegrau W., Lanka E., Barth P.T., Figurski D.H., Guiney D.G., Has D., Helinski D.R., Schwab H., Stanisich V.A., Thomas C.M.;
RT "Complete nucleotide sequence of Birmingham Incp-alpha plasmids: compilation and comparative analysis.";
RT J. Mol. Biol. 239:623-663(1994).
RN [9]
SEQUENCE FROM N.A.
RC PLASMID=R64;
RA Sampaio G., Komano T., Sasaki T., Tachibana K., Furuya N., Saito Y., Suzuki T., Mizobuchi K.;
RT "Organization and diversification of plasmid genomes: complete nucleotide sequence of R64 genome.";
RT Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [10]
SEQUENCE FROM N.A.
RC PLASMID=R64;
RX MEDLINE=87146423; PubMed=3029698;
RA Komano T., Kubo A., Nishioka T.;
RT "Shufflon: multi-inversion of four contiguous DNA segments of plasmid R64 creates seven different open reading frames.";
RT
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RP SEQUENCE FROM N.A.
RC STRAIN=drd-11; PLASMID=R64;
RX MEDLINE=91177811; PubMed=1848841;
RA Furuya N., Nishioka T., Komano T.;
RT "Nucleotide sequence and functions of the orit operon in IncII plasmid R64.";
RT J. Bacteriol. 173:2231-2237(1991).
RN [3]
SEQUENCE FROM N.A.
RC STRAIN=drd-11; PLASMID=R64;
RA Komano T., Narahara K., Yoshida T., Furuya N.;
RT "The transfer region of IncII plasmid R64: similarities between R64 tra genes and Legionella icm/dot genes.";
RT Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
SEQUENCE FROM N.A.
RC STRAIN=drd-11; PLASMID=R64;
RX MEDLINE=92011438; PubMed=1917882;
RA Furuya N., Komano T.;
RT "Determination of the nick site at orit of IncII plasmid R64: global similarity of orit structures of IncII and INCP plasmids.";
RT J. Bacteriol. 173:6612-6617(1991).
RN [5]
SEQUENCE FROM N.A.
RC STRAIN=drd-11; PLASMID=R64;
RX MEDLINE=98053841; PubMed=9393692;
RA Furuya N., Komano T.;
RT "Mutational analysis of the R64 orit region: requirement for precise location of the Nika-binding sequence.";
RT J. Bacteriol. 179:7291-7297(1997).
RN [6]
SEQUENCE FROM N.A.
RC STRAIN=drd-11; PLASMID=R64;
RX MEDLINE=98268996; PubMed=9603870;
RA Yoshida T., Furuya N., Ishikura M., Isobe T., Haino-Fukushima K., Ogawa T., Komano T.;
RT "Purification and characterization of thin pili of IncII plasmids Colib-P9 and R64: formation of Pili-specific cell aggregates by type IV pili.";
RT J. Bacteriol. 180:2842-2848(1998).
RN [7]
SEQUENCE FROM N.A.
RC STRAIN=drd-11; PLASMID=R64;
RX MEDLINE=94132048; PubMed=8300611;
RA Pansegrau W., Schroder W., Lanka E.;
RT "Concerted action of three distinct domains in the DNA cleaving-joining reaction catalyzed by relaxase (TraI) of conjugative plasmid RP4.";
RT J. Biol. Chem. 269:2782-2789(1994).
RN [8]
SEQUENCE FROM N.A.
RC STRAIN=drd-11; PLASMID=R64;
RX MEDLINE=94285211; PubMed=8014987;
RA Pansegrau W., Lanka E., Barth P.T., Figurski D.H., Guiney D.G., Has D., Helinski D.R., Schwab H., Stanisich V.A., Thomas C.M.;
RT "Complete nucleotide sequence of Birmingham Incp-alpha plasmids: compilation and comparative analysis.";
RT J. Mol. Biol. 239:623-663(1994).
RN [9]
SEQUENCE FROM N.A.
RC PLASMID=R64;
RA Sampaio G., Komano T., Sasaki T., Tachibana K., Furuya N., Saito Y., Suzuki T., Mizobuchi K.;
RT "Organization and diversification of plasmid genomes: complete nucleotide sequence of R64 genome.";
RT Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [10]
SEQUENCE FROM N.A.
RC PLASMID=R64;
RX MEDLINE=87146423; PubMed=3029698;
RA Komano T., Kubo A., Nishioka T.;
RT "Shufflon: multi-inversion of four contiguous DNA segments of plasmid R64 creates seven different open reading frames.";
RT
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RL Nucleic Acids Res. 15:1165-1172(1987).
RN [11]
RP SEQUENCE FROM N.A.
RC PLASMID=R64;
RX MEDLINE=89127142; PubMed=3065610;
RA Kubo A., Kusukawa A., Komano T.;
RT "Nucleotide sequence of the rsi gene encoding shufflon-specific DNA
RT recombinaise in the IncII plasmid R64: homology to the site-specific
RL Mol. Gen. Genet. 213:30-35(1988).
RN [12]
RP SEQUENCE FROM N.A.
RC PLASMID=R64;
RX MEDLINE=88314948; PubMed=3045094;
RA Komano T., Toyoshima A., Morita K., Nishioka T.;
RT "Cloning and nucleotide sequence of the oriI region of the IncII
RT plasmid R64.";
RL J. Bacteriol. 170:4385-4387(1988).
RN [13]
RP SEQUENCE FROM N.A.
RC PLASMID=R64;
RX MEDLINE=93352408; PubMed=8349545;
RA Kim S.R., Funayama N., Komano T.;
RT "Nucleotide sequence and characterization of the traABCD region of
RT IncII plasmid R64.";
RL J. Bacteriol. 175:5035-5042(1993).
RN [14]
RP SEQUENCE FROM N.A.
RC PLASMID=R64;
RX MEDLINE=95083745; PubMed=7991676;
RA Furuya N., Komano T.;
RT "Surface exclusion gene of IncII plasmid R64: nucleotide sequence and
RT analysis of deletion mutants.";
RL plasmid 32:80-84(1994).
RN [15]
RP SEQUENCE FROM N.A.
RC PLASMID=R64;
RX MEDLINE=97428559; PubMed=9281491;
RA Narahara K., Rahman E., Furuya N., Komano T.;
RT "Requirement of a limited segment of the sog gene for plasmid R64
RT cojugation.";
RL plasmid 38:1-11(1997).
RN [16]
RP SEQUENCE FROM N.A.
RC PLASMID=R64;
RX MEDLINE=97315231; PubMed=9171405;
RA Kim S.R., Komano T.;
RT "The plasmid R64 thin pilus identified as a type IV pilus.";
RL J. Bacteriol. 179:3594-3603(1997).
RN [17]
RP SEQUENCE FROM N.A.
RC PLASMID=R64;
RX MEDLINE=20223621; PubMed=10760136;
RA Komano T., Yoshida T., Narahara K., Furuya N.;
RT "The transfer region of IncII plasmid R64: similarities between R64
RT tra genes and Legionella icm/dot genes.";
RL Mol. Microbiol. 35:1348-1359(2000).
DR EMBL; AB027308; BAA78021.1; -
DR EMBL; AF005147; BAB91644.1; -
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR InterPro; IPR005094; Relaxase.
DR Pfam; PF03432; Relaxase; 1.
RW Plasmid.
SQ SEQUENCE 899 AA; 104010 MW; C062A360B275C337 CRC64;

Query Match 9.8%; Score 83; DB 2; Length 899;
Best Local Similarity 22.5%; Pred. No. 10;
Matches 34; Conservative 22; Mismatches 55; Indels 40; Gaps 7;

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DB SSSQAEQPHRSRSLVDYATLRN-----ESFVALVDVMDGCEWVNFYGVTCFHNCT 91
QY 84 LKSANTGNNERIINVSIIKKLRKPPSTNAGRQKRL---TCP-----SCDSYKPKPK 134
DB SLETAADMEYI-----ARQAHYAKDDTDPVFHYILSWQSHESPRPE 133
QY 135 EFLERFKSLLOKM---IHQHLSSRTHGSEDS 162
DB QIYDSVRHTLKSGLADHQYVSA-VHTDTDN 163

RESULT 9
Q9R2J7 PRELIMINARY; PRT; 899 AA.
AC Q9R2J7;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Relaxase.
GN NIKB.
OS Shigella sonnei.
OG Plasmid Colib-P9.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=624;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=P9;
RA Sampei G., Mizobuchi K.;
RT "Organization and diversification of plasmid genomes: complete
RT nucleotide sequence of the Colib-P9 genome.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB021078; BAA75140.1; -
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR InterPro; IPR005094; Relaxase.
DR Pfam; PF03432; Relaxase; 1.
RW Plasmid.
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Query Match 9.8%; Score 83; DB 2; Length 899;
Best Local Similarity 22.5%; Pred. No. 10;
Matches 34; Conservative 22; Mismatches 55; Indels 40; Gaps 7;

QY 27 SSSQGDHMIEMRQLIIVOLKNYNDLVPPELPAPEDVETNCWSAF---SCFQKAQ 83
DB SSSQAEQPHRSRSLVDYATLRN-----ESFVALVDVMDGCEWVNFYGVTCFHNCT 91
QY 84 LKSANTGNNERIINVSIIKKLRKPPSTNAGRQKRL---TCP-----SCDSYKPKPK 134
DB SLETAADMEYI-----ARQAHYAKDDTDPVFHYILSWQSHESPRPE 133
QY 135 EFLERFKSLLOKM---IHQHLSSRTHGSEDS 162
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RESULT 10
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AC Q8CPT9;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE ATP-dependent nuclease subunit A.
GN SE0664.
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12228;
RA Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
RA Chen Z., Wen Y.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE016746; AAO04261.1; -

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Db 129 RKPPEEHKKRGKPKVPKMPHTCYECHKSFKCIQAULTQHI--RHTTGE 173

Search completed: March 3, 2004, 12:38:09
Job time : 28.4706 secs

Db 24 VICNNCIYRLGVAFHFKQECNSD---LRLQVYLIGLESWR-----QDAAT 66
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Db 67 NTD-----FVEKPLLPQSDSEEEFVDAKVK-----RCSR-----YQ 99
QY 130 KPPKPEFLERFKSLLOKMIH-----OHLSSRTHGSE 160
Db 100 RKPPEEHKKRGKPKVPKMPHTCYECHKSFKCIQAULTQHI--RHTTGE 144

RESULT 15
Q9NK60 PRELIMINARY; PRT; 414 AA.
AC Q9NK60;
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE BG:DS02740.8 protein.
GN BG:DS02740.8 OR C017328.
OS Drosophila melanogaster. (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RX MEDLINE=99403001; PubMed=10471707;
RA Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T.,
RA Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,
RA Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
RA Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K.,
RA Calniker S., Rubin G.M.;
RA "An exploration of the sequence of a 2.9-Mb region of the genome of
RT Drosophila melanogaster: the Adh region.";
RL Genetics 153:179-219(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RA Calniker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G.,
RA Butenoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,
RA Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
RA Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
RA Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
RA Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
RA Sethi H., Snair E., Svirekas R.R., Wan K.H., Weinburg T., Zhang R.,
RA Zieran L.L., Rubin G.M.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003415; AAF4998.1; -
DR HSP; P08046; IAL1.
DR FlyBase; FBgn002895; BG:DS02740.8.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF00096; zf-C2H2; 6.
DR SMART; SM00355; Znf_C2H2; 6.
DR PROSITE; PS00190; CYTOCHROME C; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 6.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 6.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 414 AA; 47307 MW; 182657C92E2E2D1F CRC64;

Query Match 9.5%; Score 81; DB 5; Length 414;
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QY 70 NCEWSAFSCFQKAQLKSGANTGNNERIINVSIXKLRKPPSTNAGRQKHRLTCPSCDYSYE 129

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OM protein - protein search, using sw model

Run on: March 3, 2004, 12:33:10 ; Search time 11.3824 Seconds
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734.770 Million cell updates/sec

Title: US-09-825-561A-10

Perfect score: 850

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Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	850	100.0	162	4	US-09-923-246-2
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4	695.5	81.8	519	4	US-09-522-217-85
5	695.5	81.8	519	4	US-09-923-246-85
6	695.5	81.8	519	4	US-10-295-723-85
7	486	57.2	146	4	US-09-522-217-56
8	486	57.2	146	4	US-09-923-246-56
9	486	57.2	146	4	US-10-295-723-56
10	394	46.4	510	4	US-09-522-217-89
11	394	46.4	510	4	US-09-923-246-89
12	394	46.4	510	4	US-10-295-723-89
13	212	24.9	40	4	US-09-522-217-72
14	212	24.9	40	4	US-09-923-246-72
15	212	24.9	40	4	US-10-295-723-72
16	176	20.7	32	4	US-09-522-217-73
17	176	20.7	32	4	US-09-923-246-73
18	176	20.7	32	4	US-10-295-723-73
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22	99.5	11.7	114	1	US-08-726-817-3
23	99.5	11.7	114	1	US-08-504-042-6
24	99.5	11.7	114	1	US-08-504-042-12
25	99.5	11.7	114	2	US-08-725-969-3
26	99.5	11.7	114	2	US-08-794-524-3
27	99.5	11.7	114	3	US-09-189-193-3

28	99.5	11.7	114	4	US-09-462-941-20	Sequence 20, Appli
29	99.5	11.7	114	5	PCT-US94-03793-6	Sequence 6, Appli
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44	99.5	11.7	162	5	PCT-US94-03793-5	Sequence 5, Appli
45	99.5	11.7	162	5	PCT-US96-06423-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-522-217-2
; Sequence 2, Application US/09522217
; Patent No. 6307024
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: No. 6307024ak, Julia E.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAL1 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/522,217
; EARLIER FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: US 60/123,547
; EARLIER FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: US 60/123,904
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: US 60/142,013
; EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 162
; TYPE: PPT
; ORGANISM: Homo sapiens
US-09-522-217-2

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Best Local Similarity 100.0%; Pred. No. 1e-86;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	61	LPAPEDVETNCWSAFSCFQKAQLKSANTGNNRINVSIKLKKPKPTNAGRQKHL	120
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RESULT 2
US-09-923-246-2
; Sequence 2, Application US/09923246
; Patent No. 6605272
; GENERAL INFORMATION:
; APPLICANT: No. 6605272ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHALL LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-246-2
Query Match 100.0%; Score 850; DB 4; Length 162;
Best Local Similarity 100.0%; Pred. No. 1e-86;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
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; Patent No. 6307024
; GENERAL INFORMATION:
; APPLICANT: No. 6307024ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHALL LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/522,217
; CURRENT FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: US 60/123,547
; EARLIER FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: US 60/123,904
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: US 60/142,013
; EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
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; LENGTH: 519
; TYPE: PRT
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US-09-522-217-85
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Best Local Similarity 95.7%; Pred. No. 6.7e-69;
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QY 23 LVHKSSQGDHMRIRQLIDIVDQIKNYVNDLVPEFLPAPEDVTNCWSAFSCFQKA 82
Db 383 LVPRGS---QDRHMRIRQLIDIVDQIKNYVNDLVPEFLPAPEDVTNCWSAFSCFQKA 439
QY 83 QLKXSANTGNNERIINVSIKLKKPKPSTNAGRQKHLTCPSCDSYEKKPKPFLEFRFKS 142

US-09-923-246-2
Query Match 100.0%; Score 850; DB 4; Length 162;
Best Local Similarity 100.0%; Pred. No. 1e-86;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSPGNMRIVICLMVIFLGLTVHKSSQGDHMRIRQLIDIVDQIKNYVNDLVPEF 60
Db 1 MRSSPGNMRIVICLMVIFLGLTVHKSSQGDHMRIRQLIDIVDQIKNYVNDLVPEF 60
QY 61 LPAPEDVTNCWSAFSCFQKALXSANTGNNERIINVSIKLKKPKPSTNAGRQKHL 120
Db 61 LPAPEDVTNCWSAFSCFQKALXSANTGNNERIINVSIKLKKPKPSTNAGRQKHL 120
QY 121 TCPSCDSYEKKPKPFLEFRFKSLLOQMTHOHLSSRTHSEDS 162
Db 121 TCPSCDSYEKKPKPFLEFRFKSLLOQMTHOHLSSRTHSEDS 162

RESULT 3
US-10-295-723-2
; Sequence 2, Application US/10295723
; Patent No. 6686178
; GENERAL INFORMATION:
; APPLICANT: No. 6686178ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHALL LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
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DB      440 QLKSA NTGN NRI I NVSI K L K R K P P S T N A G R Q K H L T C P S C D S Y E K K P P K E F L E R F K S      499
DY      143 L L Q K M I H Q L S R T H G S E D S      162
DB      500 L L Q K M I H Q L S R T H G S E D S      519

RESULT 5
US-09-923-246-85
; Sequence 85, Application US/09923246
; Patent No. 6605272
; GENERAL INFORMATION:
; APPLICANT: No. 6605272ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHALL LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PastSeq for Windows Version 3.0
; SEQ ID NO 85
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MBP-human zalphall Ligand fusion polypeptide
US-09-923-246-85

Query Match      81.8%; Score 695.5; DB 4; Length 519;
Best Local Similarity 95.7%; Pred. No. 6.7e-69;
Matches 134; Conservative 1; Mismatches 2; Indels 3; Gaps 1

QY      23 LVHKSSQSQDRHLMRMQLDIVDLQKNYNDLVPEFLPAPEVDVNTCEWSAFSCFQKA      82
DB      383 LVFRGS---QDRHLMRMQLDIVDLQKNYNDLVPEFLPAPEVDVNTCEWSAFSCFQKA      439
QY      83 QLKSA NTGN NRI I NVSI K L K R K P P S T N A G R Q K H L T C P S C D S Y E K K P P K E F L E R F K S      142
DB      440 QLKSA NTGN NRI I NVSI K L K R K P P S T N A G R Q K H L T C P S C D S Y E K K P P K E F L E R F K S      499
QY      143 L L Q K M I H Q L S R T H G S E D S      162
DB      500 L L Q K M I H Q L S R T H G S E D S      519

RESULT 6
US-10-295-723-85
; Sequence 85, Application US/10295723
; Patent No. 6686178
; GENERAL INFORMATION:
; APPLICANT: No. 6686178ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.

```

```
Query Match 57.2%; Score 486; DB 4; Length 146;
Best Local Similarity 63.0%; Pred. No. 2.5e-46;
Matches 92; Conservative 23; Mismatches 31; Indels 0; Gaps 0;

QY 8 MERIVICLVIFLGTIVHKSOGQDRHMIRMQRLIDIVDQKKNVNDLVPEFLPAPEDV 67
DB 1 MERTVCLVIFLGTIVHKSOGQDRHLLRLRHLDIVDQKKNVNDLVPEFLPAPEDV 60
QY 68 ETNCWSAFSCFQKALKSANTGNRIINVS:KKLKRPPSTNAGRQKRLTSPSCDS 127
DB 61 KGHCEHAFAFCQKALKPSNPGNNKTFIIDLVQALRRRLPARRGGKKQKHIAKCPSCDS 120
QY 128 YEKKPPKEFLERFKSLQKMIHQHLS 153
DB 121 YEKRTPKFLERLKWLQKMIHQHLS 146

RESULT 8
US-09-923-246-56
; Sequence 56, Application US/0923246
; Patent No. 6605272
; GENERAL INFORMATION:
; APPLICANT: No. 6605272ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 56
; LENGTH: 146
; TYPE: PRT
; ORGANISM: mus musculus
US-09-923-246-56

Query Match 57.2%; Score 486; DB 4; Length 146;
Best Local Similarity 63.0%; Pred. No. 2.5e-46;
Matches 92; Conservative 23; Mismatches 31; Indels 0; Gaps 0;

QY 8 MERIVICLVIFLGTIVHKSOGQDRHMIRMQRLIDIVDQKKNVNDLVPEFLPAPEDV 67
DB 1 MERTVCLVIFLGTIVHKSOGQDRHLLRLRHLDIVDQKKNVNDLVPEFLPAPEDV 60
QY 68 ETNCWSAFSCFQKALKSANTGNRIINVS:KKLKRPPSTNAGRQKRLTSPSCDS 127
DB 61 KGHCEHAFAFCQKALKPSNPGNNKTFIIDLVQALRRRLPARRGGKKQKHIAKCPSCDS 120
QY 128 YEKKPPKEFLERFKSLQKMIHQHLS 153
DB 121 YEKRTPKFLERLKWLQKMIHQHLS 146

RESULT 9
US-10-295-723-56
; Sequence 56, Application US/10295723
; Patent No. 6686178
; GENERAL INFORMATION:
; APPLICANT: No. 6686178ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/522,217
; CURRENT FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; EARLIER FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: US 60/123,904
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: US 60/142,013
; EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
```

```
APPLICANT: No. 6686178ak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/10/295,723
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: 09/522,217
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: US 60/123,547
PRIOR FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 60/142,013
PRIOR FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 56
LENGTH: 146
TYPE: PRT
ORGANISM: mus musculus
US-10-295-723-56

Query Match 57.2%; Score 486; DB 4; Length 146;
Best Local Similarity 63.0%; Pred. No. 2.5e-46;
Matches 92; Conservative 23; Mismatches 31; Indels 0; Gaps 0;

QY 8 MERIVICLVIFLGTIVHKSOGQDRHMIRMQRLIDIVDQKKNVNDLVPEFLPAPEDV 67
DB 1 MERTVCLVIFLGTIVHKSOGQDRHLLRLRHLDIVDQKKNVNDLVPEFLPAPEDV 60
QY 68 ETNCWSAFSCFQKALKSANTGNRIINVS:KKLKRPPSTNAGRQKRLTSPSCDS 127
DB 61 KGHCEHAFAFCQKALKPSNPGNNKTFIIDLVQALRRRLPARRGGKKQKHIAKCPSCDS 120
QY 128 YEKKPPKEFLERFKSLQKMIHQHLS 153
DB 121 YEKRTPKFLERLKWLQKMIHQHLS 146

RESULT 10
US-09-522-217-89
; Sequence 89, Application US/09522217
; Patent No. 6307024
; GENERAL INFORMATION:
; APPLICANT: No. 6307024ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/522,217
; CURRENT FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; EARLIER FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: US 60/123,904
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: US 60/142,013
; EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
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SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 89

LENGTH: 510

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: MBP-mouse zalphall1 Ligand fusion polypeptide

US-09-522-217-89

Query Match 46.4%; Score 394; DB 4; Length 510;

Best Local Similarity 62.0%; Pred. No. 2e-35;

Matches 75; Conservative 19; Mismatches 27; Indels 0; Gaps 0;

QY 33 DRHMIRQLDIDVQLKYNVNDLPFLPAPEDVETNCWSAFSCFQKALKSANTGNN 92

DB 390 DRLIRLRHLIDIVQLKIYENDLPDLSAPQDVKGCHHAFAAFQKAKLPSPNGNN 449

QY 93 ERIINVSIKKLKRPSTNAGRQKRLTCDSCDSYKPKPKPEFLERFKSLQKMIHOHL 152

DB 450 KTFIIDLVAQLRRRLPARRGGKKQKHIACPCSDSYEKRTPKPEFLERLKLWLLQKMIHOHL 509

QY 153 S 153

DB 510 S 510

RESULT 11

US-09-923-246-89

Sequence 89, Application US/09923246

Patent No. 6605272

GENERAL INFORMATION:

APPLICANT: No. 6605272ak, Julia E.

APPLICANT: Presnell, Scott R.

APPLICANT: Sprecher, Cindy A.

APPLICANT: Foster, Donald C.

APPLICANT: Holly, Richard D.

APPLICANT: Gross, Jane A.

APPLICANT: Johnston, Janet V.

APPLICANT: Nelson, Andrew J.

APPLICANT: Dillon, Stacey R.

APPLICANT: Hammond, Angela K.

TITLE OF INVENTION: NOVEL CYTOKINE ZALPHALL1 LIGAND

FILE REFERENCE: 99-16

CURRENT APPLICATION NUMBER: US/09/923,246

PRIOR FILING DATE: 2001-08-03

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217

PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904

PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013

PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01

NUMBER OF SEQ ID NOS: 115

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 89

LENGTH: 510

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: MBP-mouse zalphall1 Ligand fusion polypeptide

US-09-923-246-89

Query Match 46.4%; Score 394; DB 4; Length 510;

Best Local Similarity 62.0%; Pred. No. 2e-35;

Matches 75; Conservative 19; Mismatches 27; Indels 0; Gaps 0;

QY 33 DRHMIRQLDIDVQLKYNVNDLPFLPAPEDVETNCWSAFSCFQKALKSANTGNN 92

DB 390 DRLIRLRHLIDIVQLKIYENDLPDLSAPQDVKGCHHAFAAFQKAKLPSPNGNN 449

QY 93 ERIINVSIKKLKRPSTNAGRQKRLTCDSCDSYKPKPKPEFLERFKSLQKMIHOHL 152

DB 450 KTFIIDLVAQLRRRLPARRGGKKQKHIACPCSDSYEKRTPKPEFLERLKLWLLQKMIHOHL 509

QY 153 S 153

DB 510 S 510

RESULT 12

US-10-295-723-89

Sequence 89, Application US/10295723

Patent No. 6686178

GENERAL INFORMATION:

APPLICANT: No. 6686178ak, Julia E.

APPLICANT: Presnell, Scott R.

APPLICANT: Sprecher, Cindy A.

APPLICANT: Foster, Donald C.

APPLICANT: Holly, Richard D.

APPLICANT: Gross, Jane A.

APPLICANT: Johnston, Janet V.

APPLICANT: Nelson, Andrew J.

APPLICANT: Dillon, Stacey R.

APPLICANT: Hammond, Angela K.

TITLE OF INVENTION: NOVEL CYTOKINE ZALPHALL1 LIGAND

FILE REFERENCE: 99-16

CURRENT APPLICATION NUMBER: US/10/295,723

PRIOR FILING DATE: 2002-11-15

PRIOR APPLICATION NUMBER: 09/522,217

PRIOR FILING DATE: 2000-03-09

PRIOR APPLICATION NUMBER: US 60/123,547

PRIOR FILING DATE: 1999-03-09

PRIOR APPLICATION NUMBER: US 60/123,904

PRIOR FILING DATE: 1999-03-11

PRIOR APPLICATION NUMBER: US 60/142,013

PRIOR FILING DATE: 1999-07-01

NUMBER OF SEQ ID NOS: 115

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 89

LENGTH: 510

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: MBP-mouse zalphall1 Ligand fusion polypeptide

US-10-295-723-89

Query Match 46.4%; Score 394; DB 4; Length 510;

Best Local Similarity 62.0%; Pred. No. 2e-35;

Matches 75; Conservative 19; Mismatches 27; Indels 0; Gaps 0;

QY 33 DRHMIRQLDIDVQLKYNVNDLPFLPAPEDVETNCWSAFSCFQKALKSANTGNN 92

DB 390 DRLIRLRHLIDIVQLKIYENDLPDLSAPQDVKGCHHAFAAFQKAKLPSPNGNN 449

QY 93 ERIINVSIKKLKRPSTNAGRQKRLTCDSCDSYKPKPKPEFLERFKSLQKMIHOHL 152

DB 450 KTFIIDLVAQLRRRLPARRGGKKQKHIACPCSDSYEKRTPKPEFLERLKLWLLQKMIHOHL 509

QY 153 S 153

DB 510 S 510

RESULT 13

US-09-522-217-72

Sequence 72, Application US/09522217

Patent No. 6307024

GENERAL INFORMATION:

APPLICANT: No. 6307024ak, Julia E.

APPLICANT: Presnell, Scott R.

APPLICANT: Sprecher, Cindy A.

APPLICANT: Foster, Donald C.

APPLICANT: Holly, Richard D.

APPLICANT: Gross, Jane A.

APPLICANT: Johnston, Janet V.

APPLICANT: Nelson, Andrew J.

APPLICANT: Dillon, Stacey R.

APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/09/522,217
EARLIER APPLICATION NUMBER: US 60/123,547
EARLIER FILING DATE: 2000-03-09
EARLIER APPLICATION NUMBER: US 60/123,547
EARLIER FILING DATE: 1999-03-09
EARLIER APPLICATION NUMBER: US 60/123,904
EARLIER FILING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: US 60/142,013
EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 72
LENGTH: 40
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Huzalpalh1L-1 peptide
US-09-522-217-72

Query Match 24.9%; Score 212; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.3e-16;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 QDRHMIRQLIDIVDQKNVNDLVPEFLPAPEDVETNC 71
DB 1 QDRHMIRQLIDIVDQKNVNDLVPEFLPAPEDVETNC 40

RESULT 14
US-09-923-246-72
Sequence 72, Application US/09923246
Patent No. 6605272
GENERAL INFORMATION:
APPLICANT: No. 6605272ak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/09/923,246
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 72
LENGTH: 40
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Huzalpalh1L-1 peptide
US-09-923-246-72

Query Match 24.9%; Score 212; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.3e-16;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 QDRHMIRQLIDIVDQKNVNDLVPEFLPAPEDVETNC 71
DB 1 QDRHMIRQLIDIVDQKNVNDLVPEFLPAPEDVETNC 40

RESULT 15
US-10-295-723-72
Sequence 72, Application US/10295723
Patent No. 6686178
GENERAL INFORMATION:
APPLICANT: No. 6686178ak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/10/295,723
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: 09/522,217
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: US 60/123,547
PRIOR FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 60/142,013
PRIOR FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 72
LENGTH: 40
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Huzalpalh1L-1 peptide
US-10-295-723-72

Query Match 24.9%; Score 212; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.3e-16;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 QDRHMIRQLIDIVDQKNVNDLVPEFLPAPEDVETNC 71
DB 1 QDRHMIRQLIDIVDQKNVNDLVPEFLPAPEDVETNC 40

Search completed: March 3, 2004, 12:39:56
Job time : 12.3824 secs

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OM protein - protein search, using sw model

Run on: March 3, 2004, 12:38:15 ; Search time 21.1765 Seconds
(without alignments)
1615.322 Million cell updates/sec

Title: US-09-825-561A-10
Perfect score: 850
Sequence: 1 MRSSPGNMRIVICLWIFL.....LLQXIHHLSSRTHGSEDS 162

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
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2: /cgm2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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8: /cgm2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgm2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgm2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgm2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgm2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgm2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgm2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgm2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgm2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
17: /cgm2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgm2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	850	100.0	162	9	US-09-923-246-2
2	850	100.0	162	9	US-09-825-561A-10
3	850	100.0	162	10	US-09-972-218A-19
4	850	100.0	162	14	US-10-264-634-19
5	850	100.0	162	14	US-10-295-723-2
6	850	100.0	162	14	US-10-282-622-2
7	850	100.0	162	15	US-10-456-780-2
8	831	97.8	162	14	US-10-282-622-6
9	758	89.2	147	14	US-10-282-622-4
10	695.5	81.8	519	9	US-09-923-246-85
11	695.5	81.8	519	14	US-10-295-723-85
12	486	57.2	146	9	US-09-825-246-56
13	486	57.2	146	9	US-09-825-561A-47
14	486	57.2	146	14	US-10-295-723-56
15	486	57.2	146	15	US-10-456-780-4

16	394	46.4	510	9	US-09-923-246-89	Sequence 89, Appl
17	394	46.4	510	14	US-10-295-723-89	Sequence 89, Appl
18	212	24.9	40	9	US-09-923-246-72	Sequence 72, Appl
19	212	24.9	40	14	US-10-235-723-72	Sequence 72, Appl
20	176	20.7	32	9	US-09-923-246-73	Sequence 73, Appl
21	176	20.7	32	14	US-10-295-723-73	Sequence 73, Appl
22	99.5	11.7	114	14	US-10-400-377-20	Sequence 20, Appl
23	99.5	11.7	114	14	US-10-400-708-20	Sequence 20, Appl
24	99.5	11.7	114	14	US-10-298-148-20	Sequence 20, Appl
25	99.5	11.7	162	9	US-09-953-323A-4	Sequence 4, Appl
26	99.5	11.7	162	9	US-09-953-323A-4	Sequence 4, Appl
27	99.5	11.7	162	9	US-09-923-246-113	Sequence 113, Appl
28	99.5	11.7	162	14	US-10-245-243-6	Sequence 6, Appl
29	99.5	11.7	162	14	US-10-295-723-113	Sequence 113, Appl
30	99.5	11.7	162	14	US-10-282-622-9	Sequence 9, Appl
31	99.5	11.7	162	15	US-10-456-780-9	Sequence 9, Appl
32	99.5	11.7	162	16	US-10-275-620-2	Sequence 2, Appl
33	94.5	11.1	122	14	US-10-385-072-3	Sequence 3, Appl
34	94.5	11.1	162	9	US-09-953-323A-2	Sequence 2, Appl
35	94.5	11.1	162	9	US-09-855-313A-2	Sequence 8, Appl
36	94.5	11.1	162	14	US-10-245-243-8	Sequence 6, Appl
37	91.5	10.8	337	9	US-09-899-980A-6	Sequence 48, Appl
38	91.5	10.8	337	14	US-10-004-633-48	Sequence 48, Appl
39	91.5	10.8	337	14	US-10-004-633-49	Sequence 49, Appl
40	91.5	10.8	342	14	US-10-004-633-41	Sequence 41, Appl
41	91.5	10.8	567	9	US-09-899-980A-7	Sequence 7, Appl
42	91.5	10.8	567	14	US-10-011-548-34	Sequence 24, Appl
43	91.5	10.8	567	14	US-10-004-633-39	Sequence 39, Appl
44	77	9.1	139	14	US-10-101-464A-639	Sequence 639, Appl
45	76	8.9	400	14	US-10-101-464A-939	Sequence 939, Appl

ALIGNMENTS

RESULT 1

US-09-923-246-2
; Sequence 2, Application US/09923246
; Patent No. US20020128446A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020128446Alak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 2000-03-09
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-03-11
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-07-01
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-246-2

Query Match 100.0%; Score 850; DB 9; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.8e-84;
Matches 162; Conservative 0; Indels 0; Gaps 0;

1 MRSSPGNMRIVICLWIFLVLGTVLHKSSGQDRHMRQLDVLQKYNVDLVPF 60

Db 1 MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMRQLDIVDQKKNYNDLVPEF 60
QY 61 LPAPEDVETNCWSAFSCFQKQKSAKNTGNRRINVSIIKKLKKPPSTNAGRRQKHL 120
Db 61 LPAPEDVETNCWSAFSCFQKQKSAKNTGNRRINVSIIKKLKKPPSTNAGRRQKHL 120
QY 121 TCPSCDSYEKKPKPEFLERFKSLLOKMIHQHLSRTHGSEDS 162
Db 121 TCPSCDSYEKKPKPEFLERFKSLLOKMIHQHLSRTHGSEDS 162

RESULT 2

US-09-825-561A-10
; Sequence 10, Application US/09825561A
; Patent No. US20020137677A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. US20020137677A1ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR FILING DATE: 2000-04-05
; PRIOR FILING DATE: 2000-04-05
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-561A-10

Query Match 100.0%; Score 850; DB 9; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.8e-84;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMRQLDIVDQKKNYNDLVPEF 60
Db 1 MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMRQLDIVDQKKNYNDLVPEF 60
QY 61 LPAPEDVETNCWSAFSCFQKQKSAKNTGNRRINVSIIKKLKKPPSTNAGRRQKHL 120
Db 61 LPAPEDVETNCWSAFSCFQKQKSAKNTGNRRINVSIIKKLKKPPSTNAGRRQKHL 120
QY 121 TCPSCDSYEKKPKPEFLERFKSLLOKMIHQHLSRTHGSEDS 162
Db 121 TCPSCDSYEKKPKPEFLERFKSLLOKMIHQHLSRTHGSEDS 162

RESULT 3

US-09-972-218A-19
; Sequence 19, Application US/09972218A
; Publication No. US20030049798A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Laura
; APPLICANT: Whitters, Matthew J
; APPLICANT: Collins, Mary
; APPLICANT: Young, Deborah A.
; APPLICANT: Donaldson, Debra D.
; APPLICANT: Lowe, Leslie D.
; APPLICANT: Unger, Michelle
; TITLE OF INVENTION: MU-1, Member of the Cytokine Receptor Family
; FILE REFERENCE: 22058-552CIP2
; CURRENT APPLICATION NUMBER: US/09/972,218A
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: 09/569384

; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: 09/560766
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US/6057128
; PRIOR FILING DATE: 1998-03-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 19
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Human
US-09-972-218A-19

Query Match 100.0%; Score 850; DB 10; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.8e-84;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMRQLDIVDQKKNYNDLVPEF 60
Db 1 MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMRQLDIVDQKKNYNDLVPEF 60
QY 61 LPAPEDVETNCWSAFSCFQKQKSAKNTGNRRINVSIIKKLKKPPSTNAGRRQKHL 120
Db 61 LPAPEDVETNCWSAFSCFQKQKSAKNTGNRRINVSIIKKLKKPPSTNAGRRQKHL 120
QY 121 TCPSCDSYEKKPKPEFLERFKSLLOKMIHQHLSRTHGSEDS 162
Db 121 TCPSCDSYEKKPKPEFLERFKSLLOKMIHQHLSRTHGSEDS 162

RESULT 4

US-10-264-634-19
; Sequence 19, Application US/10264634
; Publication No. US20030108549A1
; GENERAL INFORMATION:
; APPLICANT: Donaldson, Debra et al.
; TITLE OF INVENTION: Methods and Compositions for Modulating Interleukin-21 Receptor ;
; FILE REFERENCE: G13320-F3
; CURRENT APPLICATION NUMBER: US/10/264,634
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: 09/040,005
; PRIOR FILING DATE: 1998-03-17
; PRIOR APPLICATION NUMBER: 09/560,766
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/569,384
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: 09/972,218
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/373,746
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 19
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Human
US-10-264-634-19

Query Match 100.0%; Score 850; DB 14; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.8e-84;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMRQLDIVDQKKNYNDLVPEF 60
Db 1 MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMRQLDIVDQKKNYNDLVPEF 60
QY 61 LPAPEDVETNCWSAFSCFQKQKSAKNTGNRRINVSIIKKLKKPPSTNAGRRQKHL 120
Db 61 LPAPEDVETNCWSAFSCFQKQKSAKNTGNRRINVSIIKKLKKPPSTNAGRRQKHL 120
QY 121 TCPSCDSYEKKPKPEFLERFKSLLOKMIHQHLSRTHGSEDS 162
Db 121 TCPSCDSYEKKPKPEFLERFKSLLOKMIHQHLSRTHGSEDS 162

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RESULT 5
US-10-295-723-2
; Sequence 2, Application US/10295723
; Publication No. US20030125524A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030125524Alak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
; PRIOR FILING DATE: 2000-03-09
; PRIOR FILING DATE: 2000-03-09
; PRIOR FILING DATE: 1999-03-09
; PRIOR FILING DATE: 1999-03-11
; PRIOR FILING DATE: 1999-07-01
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-723-2
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Query Match 100.0%; Score 850; DB 14; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.8e-84;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSPGNMERIVICLMVIFLGTLVHKSSQGDHMRMRLQIDIVDQKNVNDLVPEF 60
DB 1 MRSSPGNMERIVICLMVIFLGTLVHKSSQGDHMRMRLQIDIVDQKNVNDLVPEF 60
QY 61 LPAPEDVETNCWSAFSCFQKAQLKSANTGNNERIINVSIIKKLKKPPSTNAGRQKHRL 120
DB 61 LPAPEDVETNCWSAFSCFQKAQLKSANTGNNERIINVSIIKKLKKPPSTNAGRQKHRL 120
QY 121 TCPSCDSYEKKPKPEFLERFKSLLOKMIHQHLSRTHGSEDS 162
DB 121 TCPSCDSYEKKPKPEFLERFKSLLOKMIHQHLSRTHGSEDS 162
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RESULT 6
US-10-282-622-2
; Sequence 2, Application US/10282622
; Publication No. US20030134390A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: West, James W.
; APPLICANT: No. US20030134390Alak, Julia E.
; TITLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS
; FILE REFERENCE: 01-37
; CURRENT APPLICATION NUMBER: US/10/282,622
; CURRENT FILING DATE: 2002-10-28
; PRIOR FILING DATE: 2001-11-05
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 162
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-10-282-622-2

Query Match 100.0%; Score 850; DB 14; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.8e-84;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSPGNMERIVICLMVIFLGTLVHKSSQGDHMRMRLQIDIVDQKNVNDLVPEF 60
DB 1 MRSSPGNMERIVICLMVIFLGTLVHKSSQGDHMRMRLQIDIVDQKNVNDLVPEF 60
QY 61 LPAPEDVETNCWSAFSCFQKAQLKSANTGNNERIINVSIIKKLKKPPSTNAGRQKHRL 120
DB 61 LPAPEDVETNCWSAFSCFQKAQLKSANTGNNERIINVSIIKKLKKPPSTNAGRQKHRL 120
QY 121 TCPSCDSYEKKPKPEFLERFKSLLOKMIHQHLSRTHGSEDS 162
DB 121 TCPSCDSYEKKPKPEFLERFKSLLOKMIHQHLSRTHGSEDS 162
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RESULT 7
US-10-456-780-2
; Sequence 2, Application US/10456780
; Publication No. US20040009150A1
; GENERAL INFORMATION:
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Hughes, Steven D.
; APPLICANT: Holly, Richard D.
; TITLE OF INVENTION: USE OF IL-21 IN CANCER AND
; TITLE OF INVENTION: OTHER THERAPEUTIC APPLICATIONS
; FILE REFERENCE: 03-08
; CURRENT APPLICATION NUMBER: US/10/456,780
; CURRENT FILING DATE: 2003-06-06
; PRIOR FILING DATE: US 60/387,127
; PRIOR FILING DATE: 2002-06-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-456-780-2
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Query Match 100.0%; Score 850; DB 15; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.8e-84;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSPGNMERIVICLMVIFLGTLVHKSSQGDHMRMRLQIDIVDQKNVNDLVPEF 60
DB 1 MRSSPGNMERIVICLMVIFLGTLVHKSSQGDHMRMRLQIDIVDQKNVNDLVPEF 60
QY 61 LPAPEDVETNCWSAFSCFQKAQLKSANTGNNERIINVSIIKKLKKPPSTNAGRQKHRL 120
DB 61 LPAPEDVETNCWSAFSCFQKAQLKSANTGNNERIINVSIIKKLKKPPSTNAGRQKHRL 120
QY 121 TCPSCDSYEKKPKPEFLERFKSLLOKMIHQHLSRTHGSEDS 162
DB 121 TCPSCDSYEKKPKPEFLERFKSLLOKMIHQHLSRTHGSEDS 162
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RESULT 8
US-10-282-622-6
; Sequence 6, Application US/10282622
; Publication No. US20030134390A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: West, James W.
; APPLICANT: No. US20030134390Alak, Julia E.
; TITLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS
; FILE REFERENCE: 01-37
; CURRENT APPLICATION NUMBER: US/10/282,622
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 60/337,586
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; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: zalphall ligand Q153D/I156D
US-10-282-622-6

Query Match          97.8%; Score 831; DB 14; Length 162;
Best Local Similarity 98.1%; Pred. No. 2.1e-82;
Matches 159; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MRSSPGNMERIVICLWVIFGLTVLHKSSQGDHRMIRMRQLDIVDQLKNYVNDLVPEF 60
Db 1 MDSSPGNMERIVICLWVIFGLTVLHKSSQGDHRMIRMRQLDIVDQLKNYVNDLVPEF 60
QY 61 LPAPEDVETNCWSAFSCFQKALKSANTGNNERIINVSIKLKKPPSTNAGRQKHEL 120
Db 61 LPAPEDVETNCWSAFSCFQKALKSANTGNNERIINVSIKLKKPPSTNAGRQKHEL 120
QY 121 TCPSCDSYEKKPKPEFLERFKSLIQMVIHQHLSRTHGSEDS 162
Db 121 TCPSCDSYEKKPKPEFLERFKSLIQMVIHQHLSRTHGSEDS 162

RESULT 9
US-10-282-622-4
; Sequence 4, Application US/10282622
; Publication No. US20030134390A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: West, James W.
; APPLICANT: No. US20030134390A1ak, Julia E.
; TITLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS
; FILE REFERENCE: 01-37
; CURRENT APPLICATION NUMBER: US/10/282,622
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 60/337,586
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: zalphall ligand Q153D/I156D
US-10-282-622-4

Query Match          89.2%; Score 758; DB 14; Length 147;
Best Local Similarity 98.6%; Pred. No. 1.6e-74;
Matches 145; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRSSPGNMERIVICLWVIFGLTVLHKSSQGDHRMIRMRQLDIVDQLKNYVNDLVPEF 60
Db 1 MDSSPGNMERIVICLWVIFGLTVLHKSSQGDHRMIRMRQLDIVDQLKNYVNDLVPEF 60
QY 61 LPAPEDVETNCWSAFSCFQKALKSANTGNNERIINVSIKLKKPPSTNAGRQKHEL 120
Db 61 LPAPEDVETNCWSAFSCFQKALKSANTGNNERIINVSIKLKKPPSTNAGRQKHEL 120
QY 121 TCPSCDSYEKKPKPEFLERFKSLIQM 147
Db 121 TCPSCDSYEKKPKPEFLERFKSLIQM 147

RESULT 10
US-09-923-246-85
; Sequence 85, Application US/09923246
; Patent No. US20020128446A1
```

```

; GENERAL INFORMATION:
; APPLICANT: No. US20020128446A1ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 85
; LENGTH: 519
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MBP-human zalphall ligand fusion polypeptide
US-09-923-246-85

Query Match          81.8%; Score 695.5; DB 9; Length 519;
Best Local Similarity 95.7%; Pred. No. 5.4e-67;
Matches 134; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 23 LVKSSQSGQDRHMIRMRQLDIVDQLKNYVNDLVPEFLPAPEDVETNCWSAFSCFQKA 82
Db 383 LVPRGS---QDRHMIRMRQLDIVDQLKNYVNDLVPEFLPAPEDVETNCWSAFSCFQKA 439
QY 83 QLKXANTGNNERIINVSIKLKKPPSTNAGRQKRLTCPSCDSYEKKPKPEFLERFKS 142
Db 440 QLKXANTGNNERIINVSIKLKKPPSTNAGRQKRLTCPSCDSYEKKPKPEFLERFKS 499
QY 143 LQKMIHQHLSRTHGSEDS 162
Db 500 LQKMIHQHLSRTHGSEDS 519

RESULT 11
US-10-295-723-85
; Sequence 85, Application US/10295723
; Publication No. US2003012554A1
; GENERAL INFORMATION:
; APPLICANT: No. US2003012554A1ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
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;; PRIOR APPLICATION NUMBER: US 60/142,013
;; PRIOR FILING DATE: 1999-07-01
;; NUMBER OF SEQ ID NOS: 115
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 85
;; LENGTH: 519
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: MBP-human zalphall1 Ligand fusion polypeptide
US-10-295-723-85

Query Match 81.8%; Score 695.5; DB 14; Length 519;
Best Local Similarity 95.7%; Pred. No. 5.4e-67;
Matches 134; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 23 LVHSSSGQDHRMIRKQLDIDVDQKNYVNDLVPEFLPAPEDVETNCWSAFSCFQKA 82
DB 383 LVPRGS---QDRHMRKQLDIDVDQKNYVNDLVPEFLPAPEDVETNCWSAFSCFQKA 439

QY 83 QLKSAANTGNRIINVSIKKLRKPPSTNAGRROKHLRTPSCDSYSEKKPKPEFLERPKS 142
DB 440 QLKSAANTGNRIINVSIKKLRKPPSTNAGRROKHLRTPSCDSYSEKKPKPEFLERPKS 499

QY 143 LQKMIHQHLSRTHGSDS 162
DB 500 LQKMIHQHLSRTHGSDS 519

RESULT 12
US-09-923-246-56
;; Sequence 56, Application US/09923246
;; Patent No. US20020128446A1
;; GENERAL INFORMATION:
;; APPLICANT: No. US20020128446A1ak, Julia E.
;; APPLICANT: Presnell, Scott R.
;; APPLICANT: Sprecher, Cindy A.
;; APPLICANT: Foster, Donald C.
;; APPLICANT: Holly, Richard D.
;; APPLICANT: Gross, Jane A.
;; APPLICANT: Johnston, Janet V.
;; APPLICANT: Nelson, Andrew J.
;; APPLICANT: Dillon, Stacey R.
;; APPLICANT: Hammond, Angela K.
;; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHALL1 LIGAND
;; FILE REFERENCE: 99-16
;; CURRENT APPLICATION NUMBER: US/09/923,246
;; CURRENT FILING DATE: 2001-08-03
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
;; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
;; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
;; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
;; NUMBER OF SEQ ID NOS: 115
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 56
;; LENGTH: 146
;; TYPE: PRT
;; ORGANISM: mus musculus
US-09-923-246-56

Query Match 57.2%; Score 486; DB 9; Length 146;
Best Local Similarity 63.0%; Pred. No. 6.6e-45;
Matches 92; Conservative 23; Mismatches 31; Indels 0; Gaps 0;

QY 8 MERIVICLVIFLGTLVHSSSGQDHRMIRKQLDIDVDQKNYVNDLVPEFLPAPEDV 67
DB 1 MERTLVCLVIFLGTVAHSSSGQDPRLLIRLRLHLDIVQQLKIYENDLDPILLSAPQDV 60

QY 68 ETNCEWSAFSCFQKALKSANTGNRIINVSIKKLRKPPSTNAGRROKHLRTPSCDS 127
DB 61 KGHCEHAFAFCQKALKPSNPNKTFIIDLVAQLRRRLPARGGKKQKHIACPCSDS 120

QY 128 YEKPPKEFLERFKSLQKMIHQHLS 153
DB 121 YEKTPKEFLERLKWLLQKMIHQHLS 146

RESULT 13
US-09-825-561A-47
;; Sequence 47, Application US/09825561A
;; Patent No. US20020137677A1
;; GENERAL INFORMATION:
;; APPLICANT: Sprecher, Cindy A.
;; APPLICANT: No. US20020137677A1ak, Julia E.
;; APPLICANT: West, James W.
;; APPLICANT: Presnell, Scott R.
;; APPLICANT: Holly, Richard D.
;; APPLICANT: Nelson, Andrew J.
;; TITLE OF INVENTION: SOLUBLE ZALPHALL1 CYTOKINE RECEPTORS
;; FILE REFERENCE: 00-22
;; CURRENT APPLICATION NUMBER: US/09/825,561A
;; CURRENT FILING DATE: 2000-04-05
;; PRIOR APPLICATION NUMBER: US 60/194,731
;; PRIOR FILING DATE: 2000-04-05
;; PRIOR APPLICATION NUMBER: US 60/222,121
;; PRIOR FILING DATE: 2000-07-28
;; NUMBER OF SEQ ID NOS: 86
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 47
;; LENGTH: 146
;; TYPE: PRT
;; ORGANISM: Mus musculus
US-09-825-561A-47

Query Match 57.2%; Score 486; DB 9; Length 146;
Best Local Similarity 63.0%; Pred. No. 6.6e-45;
Matches 92; Conservative 23; Mismatches 31; Indels 0; Gaps 0;

QY 8 MERIVICLVIFLGTLVHSSSGQDHRMIRKQLDIDVDQKNYVNDLVPEFLPAPEDV 67
DB 1 MERTLVCLVIFLGTVAHSSSGQDPRLLIRLRLHLDIVQQLKIYENDLDPILLSAPQDV 60

QY 68 ETNCEWSAFSCFQKALKSANTGNRIINVSIKKLRKPPSTNAGRROKHLRTPSCDS 127
DB 61 KGHCEHAFAFCQKALKPSNPNKTFIIDLVAQLRRRLPARGGKKQKHIACPCSDS 120

QY 128 YEKPPKEFLERFKSLQKMIHQHLS 153
DB 121 YEKTPKEFLERLKWLLQKMIHQHLS 146

RESULT 14
US-10-295-723-56
;; Sequence 56, Application US/10295723
;; Publication No. US20030125524A1
;; GENERAL INFORMATION:
;; APPLICANT: No. US20030125524A1ak, Julia E.
;; APPLICANT: Presnell, Scott R.
;; APPLICANT: Sprecher, Cindy A.
;; APPLICANT: Foster, Donald C.
;; APPLICANT: Holly, Richard D.
;; APPLICANT: Gross, Jane A.
;; APPLICANT: Johnston, Janet V.
;; APPLICANT: Nelson, Andrew J.
;; APPLICANT: Dillon, Stacey R.
;; APPLICANT: Hammond, Angela K.
;; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHALL1 LIGAND
;; FILE REFERENCE: 99-16
;; CURRENT APPLICATION NUMBER: US/10/295,723
;; CURRENT FILING DATE: 2002-11-15
;; PRIOR APPLICATION NUMBER: 09/522,217
;; PRIOR FILING DATE: 2000-03-09
;; PRIOR APPLICATION NUMBER: US 60/123,547
;; PRIOR FILING DATE: 1999-03-09

PRIOR APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 60/142,013
PRIOR FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 56
LENGTH: 146
TYPE: PRT
ORGANISM: mus musculus
US-10-295-723-56

Query Match 57.2%; Score 486; DB 14; Length 146;
Best Local Similarity 63.0%; Pred. No. 6.6e-45;
Matches 92; Conservative 23; Mismatches 31; Indels 0; Gaps 0;

QY 8 MERIVICLVIFLGTVAHSSQGGDRHMRQLIDIVDLKNNYNDLVPEFLPAPEDV 67
DB 1 MERTLVCLVIFLGTVAHSSQGGDRHMRQLIDIVDLKNNYNDLVPEFLPAPEDV 60
QY 68 ETNCEWAFSCFQAKLKSANTGNRIINVSIIKKRKPSTNAGRRQKRLTCPSGDS 127
DB 61 KGHCEHAFAACFQAKLKSANTGNRIINVSIIKKRKPSTNAGRRQKRLTCPSGDS 120
QY 128 YEKPPKPEFLERFKSLQKMIHQHLS 153
DB 121 YEKRTPKPEFLERLKLQKMIHQHLS 146

RESULT 15
US-10-456-780-4
Sequence 4, Application US/10456780
Publication No. US20040009150A1
GENERAL INFORMATION:
APPLICANT: Nelson, Andrew J.
APPLICANT: Hughes, Steven D.
APPLICANT: Holly, Richard D.
TITLE OF INVENTION: USE OF IL-21 IN CANCER AND
OTHER THERAPEUTIC APPLICATIONS
FILE REFERENCE: 03-08
CURRENT APPLICATION NUMBER: US/10/456,780
CURRENT FILING DATE: 2003-06-06
PRIOR APPLICATION NUMBER: US 60/387,127
PRIOR FILING DATE: 2002-06-07
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 146
TYPE: PRT
ORGANISM: Mus musculus
US-10-456-780-4

Query Match 57.2%; Score 486; DB 15; Length 146;
Best Local Similarity 63.0%; Pred. No. 6.6e-45;
Matches 92; Conservative 23; Mismatches 31; Indels 0; Gaps 0;

QY 8 MERIVICLVIFLGTVAHSSQGGDRHMRQLIDIVDLKNNYNDLVPEFLPAPEDV 67
DB 1 MERTLVCLVIFLGTVAHSSQGGDRHMRQLIDIVDLKNNYNDLVPEFLPAPEDV 60
QY 68 ETNCEWAFSCFQAKLKSANTGNRIINVSIIKKRKPSTNAGRRQKRLTCPSGDS 127
DB 61 KGHCEHAFAACFQAKLKSANTGNRIINVSIIKKRKPSTNAGRRQKRLTCPSGDS 120
QY 128 YEKPPKPEFLERFKSLQKMIHQHLS 153
DB 121 YEKRTPKPEFLERLKLQKMIHQHLS 146

Search completed: March 3, 2004, 12:50:52
Job time : 22.1765 secs

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OM protein - protein search, using sw model

Run on: March 3, 2004, 12:24:04 ; Search time 38.6471 Seconds
(without alignments)
1184.377 Million cell updates/sec

Title: US-09-825-561a-10
Perfect score: 850
Sequence: 1 MRSPGNRIVICIMVFL.....LLOKMIHLSRTHGSEDS 162

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseq1980s:*
2: geneseq1990s:*
3: geneseq2000s:*
4: geneseq2001s:*
5: geneseq2002s:*
6: geneseq2003as:*
7: geneseq2003bs:*
8: geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match	Length	DB ID	Description
1	850	100.0	162	3 AAB18623	Aab18623 A human z
2	850	100.0	162	5 AAE13729	Aae13729 Human sol
3	850	100.0	162	5 AAU11965	Aau11965 Human zal
4	850	100.0	162	6 ABR61407	Abr61407 Human IL-
5	850	100.0	162	7 AAE14932	Aae14932 Human int
6	850	100.0	162	7 ABU62893	Abu62893 Human int
7	850	100.0	162	7 ADE85808	Ade85808 Human int
8	831	97.8	162	7 AAE14934	Aae14934 Human int
9	758	89.2	147	7 AAE14933	Aae14933 Human int
10	695.5	81.8	519	3 AAB18627	Aab18627 Amino aci
11	695.5	81.8	519	5 AAU11971	Aau11971 MBP-human
12	486	57.2	146	3 AAB18624	Aab18624 A mouse z
13	486	57.2	146	5 AAE13737	Aae13737 Murine so
14	486	57.2	146	5 AAU11968	Aau11968 Mouse zal
15	486	57.2	146	7 ADE85809	Ade85809 Murine in
16	486	57.2	379	7 ADE85818	Ade85818 Murine in
17	481	56.6	146	7 ADE85806	Ade85806 Murine in
18	476	56.0	146	7 ADE85807	Ade85807 Murine in
19	476	56.0	379	7 ADE85820	Ade85820 Murine mu
20	394	46.4	510	3 AAB18628	Aab18628 Amino aci
21	394	46.4	510	5 AAU11972	Aau11972 MBP-mouse
22	212	24.9	40	3 AAB18625	Aab18625 Antigenin
23	212	24.9	40	5 AAU11969	Aau11969 Human zal
24	176	20.7	32	3 AAB18626	Aab18626 Antigenin
25	176	20.7	32	5 AAU11970	Aau11970 Human zal

26	128	15.1	25	7 ADE85813	Ade85813 Human int
27	103.5	12.2	135	3 AAY54825	Aay54825 Human int
28	103.5	12.2	135	6 ADA09334	Ada09334 Human int
29	99.5	11.7	114	2 AAR66928	Aar66928 Mammalian
30	99.5	11.7	114	2 AAR83310	Aar83310 Human int
31	99.5	11.7	114	2 AAR83435	Aar83435 Mammalian
32	99.5	11.7	114	2 AAW09099	Aaw09099 Simian ma
33	99.5	11.7	114	2 AAW07253	Aaw07253 Generic m
34	99.5	11.7	114	2 AAW39186	Aaw39186 Simian ep
35	99.5	11.7	114	2 AAY03757	Aay03757 Simian ep
36	99.5	11.7	114	3 AAY52309	Aay52309 Mature si
37	99.5	11.7	114	4 AAB62013	Aab62013 Simian ET
38	99.5	11.7	162	2 AAR66927	Aar66927 Human IL-
39	99.5	11.7	162	2 AAR83438	Aar83438 Human int
40	99.5	11.7	162	2 AAR98527	Aar98527 Human int
41	99.5	11.7	162	2 AAW09098	Aaw09098 Simian ep
42	99.5	11.7	162	2 AAW07255	Aaw07255 Human epi
43	99.5	11.7	162	2 AAW01658	Aaw01658 Human int
44	99.5	11.7	162	2 AAW37369	Aaw37369 Wild-type
45	99.5	11.7	162	2 AAW39185	Aaw39185 Simian ep

ALIGNMENTS

RESULT 1
AAB18623
XX AAB18623 standard; protein; 162 AA.
AC AAB18623;
XX
DT 22-JAN-2001 (first entry)
XX
DE A human zalphall ligand polypeptide.
XX
KW zalphall ligand; cytokine; haematopoietic cell proliferation; lymphoma;
KW tumorigenesis; leukaemia; hematopoiesis; B cell tumour.
XX
OS Homo sapiens.
XX
PN WC2000053761-A2.
XX
PD 14-SEP-2000.
XX
PF 09-MAR-2000; 2000WO-US006067.
XX
PR 09-MAR-1999; 99US-00264908.
PR 11-MAR-1999; 99US-00265992.
PR 01-JUL-1999; 99US-0142013P.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
XX Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX WPI: 2000-565600/52.
XX N-PSDB; AAR75552.
XX
XX New human cytokine, designated zalphall ligand, useful for stimulating
XX the proliferation and/or development of hematopoietic cells in vitro and
XX in vivo, and for treating tumorigenesis.
XX
XX Disclosure; Page 205-206; 256pp; English.
XX
XX The present sequence represents a human zalphall ligand polypeptide,
XX which is a cytokine. The zalphall ligand is useful for stimulating the
XX proliferation and development of hematopoietic cells in vitro and in
XX vivo. Zalphall ligand polynucleotides can be used as primers or probes
XX for cloning the zalphall gene. The zalphall ligand is useful for treating
XX tumorigenesis. A zalphall ligand-saporin fusion toxin may be used for
XX treating leukaemias and lymphomas. Antagonists against zalphall ligand
XX are useful as research reagents for characterizing ligand-receptor
XX interaction. Antagonists are also useful for inhibiting expansion,

CC proliferation, activation and differentiation of cells involved in
CC regulating hematopoiesis. The zalphall ligand may also be used to
CC stimulate an immune response against B cell tumour, a virus, a parasite
CC or a bacterium. The zalphall polypeptides, polynucleotides, antagonists,
CC agonists and antibodies are also useful for the detection, diagnosis,
CC prevention, and treatment of diseases associated with a zalphall ligand
CC genetic defect
XX
SQ Sequence 162 AA;

Query Match 100.0%; Score 850; DB 3; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.3e-86;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSPGNMERIVICLMVIFLGLTVHKSSQGGDRHMIRQLIDVDQLKYNVDLVPEF 60
DB 1 MRSSPGNMERIVICLMVIFLGLTVHKSSQGGDRHMIRQLIDVDQLKYNVDLVPEF 60

QY 61 LPAPEDVETNCEWSAFSCFOKALKSANTGNNERIINVSIKKLKRPPSTNAGRQKHL 120
DB 61 LPAPEDVETNCEWSAFSCFOKALKSANTGNNERIINVSIKKLKRPPSTNAGRQKHL 120

QY 121 TCPSCDSYEKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
DB 121 TCPSCDSYEKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162

RESULT 2
AAE13729
ID AAE13729 standard; protein; 162 AA.
XX
AC AAE13729;
DT 26-FEB-2002 (first entry)
DE Human soluble Zalphall cytokine receptor ligand protein.
XX
KW Human; Zalphall; cytokine receptor; immunosuppressive; cytostatic;
KW inflammatory disorder; haemostatic; cell proliferation; immune disorder;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
KW myasthenia gravis; systemic lupus erythematosus; SLE; diabetes; asthma;
KW ulcerative colitis; inflammatory bowel disease; Crohn's disease; sepsis;
KW viral infection.
XX
OS Homo sapiens.

Key Location/Qualifiers
Peptide 1..31
Protein 32..162
Region 41..56
Region 69..84
Region 92..105
Region 135..148
Region 136..138
/label= Helix_A
/label= Helix_B
/label= Helix_C
/label= Helix_D
/note= "Conserved region"

WO200177171-A2.
18-OCT-2001.
03-APR-2001; 2001WO-US010872.
05-APR-2000; 2000US-0194731P.
28-JUL-2000; 2000US-0222121P.
(ZIMO) ZYMOGENETICS INC.

PI Sprecher CA, Novak JE, West JW, Presnell SR, Holly RD, Nelson AJ;
XX WPI; 2002-025898/03.
DR N-PSDB; AAD22923.
XX
XX Novel soluble receptor polypeptides and polynucleotides used as cytokine
XX antagonist for stimulating ligand activity-induced proliferation of
XX hematopoietic cells and for suppressing immune response in a mammal.
XX
XX Claim 1; Page 181; 243pp; English.

XX The invention relates to an isolated soluble zalphall cytokine receptor
XX polypeptide and their cDNA molecules. Zalpha proteins are useful for
XX inhibiting or antagonising the ligand activity-induced proliferation of
XX haematopoietic cells and haematopoietic cell progenitors preferably
XX lymphoid cells which are natural killer cells or cytotoxic T cells.
XX Zalpha is useful for treating immune and inflammatory disorders, for
XX reducing proliferation of neoplastic B or T cells, for suppressing an
XX immune response in a mammal exposed to an antigen or pathogen. Zalpha is
XX useful for treating diseases that require immune regulation including
XX autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,
XX myasthenia gravis, systemic lupus erythematosus (SLE) and diabetes;
XX asthma, ulcerative colitis, inflammatory bowel disease, Crohn's disease,
XX sepsis, viral infection (dengue virus infection) and cancer. The present
XX sequence is human soluble Zalphall cytokine receptor ligand
XX Sequence 162 AA;

Query Match 100.0%; Score 850; DB 5; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.3e-86;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSPGNMERIVICLMVIFLGLTVHKSSQGGDRHMIRQLIDVDQLKYNVDLVPEF 60
DB 1 MRSSPGNMERIVICLMVIFLGLTVHKSSQGGDRHMIRQLIDVDQLKYNVDLVPEF 60

QY 61 LPAPEDVETNCEWSAFSCFOKALKSANTGNNERIINVSIKKLKRPPSTNAGRQKHL 120
DB 61 LPAPEDVETNCEWSAFSCFOKALKSANTGNNERIINVSIKKLKRPPSTNAGRQKHL 120

QY 121 TCPSCDSYEKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
DB 121 TCPSCDSYEKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162

RESULT 3
AAU11965
ID AAU11965 standard; protein; 162 AA.
XX
AC AAU11965;
DT 09-APR-2002 (first entry)
DE Human zalphall ligand polypeptide.
XX
KW Cytokine; zalphall ligand; zalphall receptor; NK cell progenitor;
KW natural killer cell proliferation; T-cell proliferation;
KW B-cell proliferation; anti-tumour response; immune system;
KW immunostimulant; cytostatic; human; hPBCS;
KW activated human peripheral blood cell.
XX
OS Homo sapiens.

Key Location/Qualifiers
Peptide 1..31
Protein 32..162
/label= Signal_peptide
/label= Mature_zalphall_Ligand

US6307024-B1.
23-OCT-2001.

PF 09-MAR-2000; 2000US-00522217.
 XX 09-MAR-1999; 99US-0123547P.
 ER 11-MAR-1999; 99US-0123904P.
 PR 01-JUL-1999; 99US-0142013P.
 XX (ZYMO) ZYMOGENETICS INC.
 XX Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
 PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
 XX WPI; 2002-040208/05.
 DR N-PSDB; AAS20637.
 XX New zalphall ligand polypeptides and polynucleotides, useful for
 PT stimulating proliferation, activation, differentiation and/or induction
 PT of inhibition of specialized cell function, or for stimulating an
 PT antigenic response.
 XX Claim 7; Col 125-126; 105pp; English.
 PS The present invention relates to the isolation of a novel cytokine,
 CC zalphall ligand and the polynucleotide encoding it. The invention also
 CC gives the sequence for the zalphall receptor and the polynucleotide
 CC encoding it. The zalphall ligand polypeptide stimulates proliferation of
 CC natural killer (NK) cells or NK cell progenitors, the activation of NK
 CC cells, proliferation of T-cells, proliferation of B-cells stimulated with
 CC anti-CD40 antibodies, stimulates an antigenic response in a mammal, and
 CC reduces proliferation of B-cells stimulated with anti-IGM antibodies. The
 CC zalphall ligand polypeptide is also useful in preparing antibodies that
 CC bind to zalphall ligand epitopes. The zalphall ligand polynucleotides can
 CC be used as probes or primers to clone regions of a zalphall ligand gene,
 CC and in gene therapy. Zalphall ligand may also be used to identify
 CC inhibitors of its activity, to enhance the generation of anti-tumour
 CC responses with or without the infusion of donor lymphocytes, and to
 CC activate or stimulate the immune system. The present sequence represents
 CC human zalphall ligand polypeptide. The cDNA encoding this is isolated
 CC from a cDNA library from activated human peripheral blood cells (hPBCCs)
 XX Sequence 162 AA;
 SQ Query Match 100.0%; Score 850; DB 5; Length 162;
 Best Local Similarity 100.0%; Pred. No. 1.3e-86;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRSSPGNMRIVICLVIFLGTLVHKSSSQGQDRHMRQLIDIVDQKYNVDLVPF 60
 DB 1 MRSSPGNMRIVICLVIFLGTLVHKSSSQGQDRHMRQLIDIVDQKYNVDLVPF 60
 QY 61 LPAPEDVETNCWSAFSCFQKQKLSANTGNRINIVSIKLRKPPSTNAGRQKRL 120
 DB 61 LPAPEDVETNCWSAFSCFQKQKLSANTGNRINIVSIKLRKPPSTNAGRQKRL 120
 QY 121 TPCSDSYKKPKPPKEFLERFKSLQWIOHLSRTHGSEDS 162
 DB 121 TPCSDSYKKPKPPKEFLERFKSLQWIOHLSRTHGSEDS 162
 RESULT 4
 ABR61407
 ID ABR61407 standard; protein; 162 AA.
 XX ABR61407;
 AC ABR61407;
 XX ABR61407;
 DT 12-AUG-2003 (first entry)
 DX Human IL-21 SEQ ID NO:19.
 DE
 XX arthritic disorder; interleukin-21; IL-21; IL-21 receptor; IL-21R;
 KW immune cell activity; cancer; infectious disorder; antirheumatic;
 KW antiarthritic; osteopathic; antipsoriatic; cytostatic; antibacterial;
 KW virucide; antiparasitic; immunosuppressive; antidiabetic; dermatological;
 KW neuroprotective; antiulcer; antiallergic; antianaemic; hepatotropic;
 KW antithyroid; antinflammatory; immune response; immune disorder;
 KW autoimmune disease; human.
 OS Homo sapiens.
 XX WO2003028630-A2.
 XX 10-APR-2003.
 XX 04-OCT-2002; 2002WO-US029839.
 XX 04-OCT-2001; 2001US-00972218.
 PR 17-APR-2002; 2002US-0373746P.
 XX (AMHP) WYETH.
 PI Carter L, Whitters MJ, Collins M, Young DA, Larsen G;
 PI Donaldson DD, Lowe LD, Dunussi K, Ma M, Witek JS, Kasaian MT;
 PI Ungar M;
 XX WPI; 2003-430146/40.
 DR N-PSDB; ACC80873.
 XX Treating or preventing arthritic disorder, cancer or infectious disorders
 PT in a subject, involves administering a modulator of interleukin-21 or its
 PT receptor which modulate immune cell activity.
 XX Disclosure; Page 37; 176pp; English.
 CC The invention relates to a novel method for treating or preventing an
 CC arthritic disorder in a subject. The method involves administering to the
 CC subject an interleukin-21 (IL-21)/IL-21 receptor (IL-21R) antagonist
 CC optionally in combination with another therapeutic agent, to inhibit or
 CC reduce immune cell activity in the subject. The method is also useful for
 CC treating or preventing cancer or an infectious disorder, in a subject, by
 CC administering IL-21/IL-21R agonist, to increase immune cell activity. The
 CC method of the invention has antirheumatic, antiarthritic, osteopathic,
 CC antipsoriatic, cytostatic, antibacterial, virucide, antiparasitic,
 CC immunosuppressive, antidiabetic, neuroprotective, dermatological,
 CC antiulcer, antiasthmatic, antiallergic, antianaemic, hepatotropic,
 CC antithyroid, and antinflammatory activity. The method is useful for
 CC treating or preventing an arthritic disorder such as rheumatoid
 CC arthritis, juvenile rheumatoid arthritis, osteoarthritis, psoriatic
 CC arthritis or ankylosing spondylitis, and also cancer such as solid
 CC tumour, soft tissue tumour or metastatic lesion, or an infectious
 CC disorder such as bacterial, viral or parasitic infection in a mammal,
 CC preferably human. A method of the invention is also useful for
 CC increasing the ability of a vaccine composition containing an antigen to
 CC elicit a protective immune response in a subject against the antigens.
 CC The antigen is from a pathogen such as virus, bacterium or protozoan, or
 CC from cancer or tumour cell antigen, or expressed on the surface of cancer
 CC cell. An alternative method of the invention is useful for modulating the
 CC activity of immune or haematopoietic cells and thus to treat or prevent a
 CC variety of immune disorders, such as autoimmune diseases, for example
 CC diabetes mellitus, multiple sclerosis, myasthenia gravis, systemic lupus
 CC erythematosus, dermatitis, ulcer, asthma, allergic asthma, anaemia,
 CC hepatitis, Graves' disease, graft versus host disease, and scleroderma.
 CC The present sequence is used in an exemplification of the invention
 XX Sequence 162 AA;
 SQ Query Match 100.0%; Score 850; DB 6; Length 162;
 Best Local Similarity 100.0%; Pred. No. 1.3e-86;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRSSPGNMRIVICLVIFLGTLVHKSSSQGQDRHMRQLIDIVDQKYNVDLVPF 60
 DB 1 MRSSPGNMRIVICLVIFLGTLVHKSSSQGQDRHMRQLIDIVDQKYNVDLVPF 60
 QY 61 LPAPEDVETNCWSAFSCFQKQKLSANTGNRINIVSIKLRKPPSTNAGRQKRL 120
 DB 61 LPAPEDVETNCWSAFSCFQKQKLSANTGNRINIVSIKLRKPPSTNAGRQKRL 120

QY 121 TCPSCDSYEKKPKPEFLERFKSLLOKMIHQHLSRTHGSEDS 162
 Db 121 TCPSCDSYEKKPKPEFLERFKSLLOKMIHQHLSRTHGSEDS 162

RESULT 5

ID AAE14932 standard; protein; 162 AA.
 AC AAE14932;

XX 27-AUG-2003 (first entry)

XX Human interleukin-21 (IL-21).

XX Interleukin-21; IL-21; antagonist; cancer; inflammatory;
 KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
 KW systemic lupus erythematosus; myasthenia gravis; diabetes; human;
 KW zaiphal1 ligand.
 XX OS Homo sapiens.

XX Key Location/Qualifiers

FT Region 41..56

FT /label= Helix_A

FT Binding-site 44

FT /note= "Important for IL-21 binding to its receptor"

FT Binding-site 47

FT /note= "Important for IL-21 binding to its receptor"

FT Region 57..68

FT /label= A/B_loop

FT Region 69..84

FT /label= Helix_B

FT Region 85..91

FT /label= B/C_loop

FT Region 92..105

FT /label= Helix_C

FT Region 106..134

FT /label= C/D_loop

FT Region 135..148

FT /label= Helix_D

FT Binding-site 135

FT /note= "Important for IL-21 binding to its receptor"

XX WO2003040313-A2.

XX 15-MAY-2003.

XX 28-OCT-2002; 2002WO-US034502.

XX 05-NOV-2001; 2001US-0337586P.

XX (ZYMO) ZYMOGENETICS INC.

XX Presnell SR, West JW, Novak JE;

XX WPI; 2003-441547/41.

XX N-PSDB; RAD47852.

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CC such as cancer, inflammatory and autoimmune disorders, including
 CC rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus,
 CC myasthenia gravis and diabetes. The polypeptides can also be used to
 CC prepare antibodies that bind IL-21 epitopes, peptides or polypeptides,
 CC and for enhancing in vivo killing of target tissues. The present sequence
 CC is human IL-21 (originally designated zaiphal1 ligand)

XX SQ Sequence 162 AA;

Query Match 100.0%; Score 850; DB 7; Length 162;

Best lcal Similarity 100.0%; Pred. No. 1.3e-86;

Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSPGNMERIVICLWIFLGLTVHKSSSQODRHMIRMQLDIVDLQKYYNDLVPEF 60

Db 1 MRSPGNMERIVICLWIFLGLTVHKSSSQODRHMIRMQLDIVDLQKYYNDLVPEF 60

QY 61 LPAPEDVETNCSEAFSCFQKAQKSNANTGNRIINVSICKLKRKPPSTNAGRQKRL 120

Db 61 LPAPEDVETNCSEAFSCFQKAQKSNANTGNRIINVSICKLKRKPPSTNAGRQKRL 120

QY 121 TCPSCDSYEKKPKPEFLERFKSLLOKMIHQHLSRTHGSEDS 162

Db 121 TCPSCDSYEKKPKPEFLERFKSLLOKMIHQHLSRTHGSEDS 162

RESULT 6

ABU62893

ID ABU62893 standard; protein; 162 AA.

XX AC ABU62893;

DT 15-SEP-2003 (first entry)

XX Human interleukin 21 (IL-21).

XX Human; MU-1; haematopoietin receptor superfamily chain; immunomodulator;
 KW cytostatic; antibacterial; virucide; antianaemic; gene therapy;
 KW haematopoiesis; anaemias; immune response; cancer; infection;
 KW transplanted organ; cytokine; receptor; interleukin 21; IL21.

XX OS Homo sapiens.

XX US2003049798-A1

XX 13-MAR-2003.

XX 04-OCT-2001; 2001US-00972218.

XX 17-MAR-1998; 98US-00040005.

XX 28-APR-2000; 2000US-00560766.

XX 11-MAY-2000; 2000US-00569384.

XX (CART/) CARTER L.

XX (WHIT/) WHITTERS M J.

XX (COLL/) COLLINS M.

XX (YOUNG/) YOUNG D A.

XX (DONA/) DONALDSON D D.

XX (LOWE/) LOWE L D.

XX (UNGE/) UNGER M.

XX Carter L, Whitters MJ, Collins M, Young DA, Donaldson DD;

XX PI Lowe LD, Unger M;

XX WPI; 2003-512354/48.

XX N-PSDB; ACD26729.

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New fusion polypeptide for regulating hematopoiesis and immune responses,
 comprises a fragment of a MU-1 polypeptide and a non-MU-1 fusion
 polypeptide.

PS Disclosure; page 10; 26pp; English.

XX

CC The invention describes a fusion polypeptide comprising at least a
 CC fragment of a MU-1 polypeptide and a non-MU-1 fusion polypeptide. The
 CC polypeptide is useful in regulating haematopoiesis (e.g. in cases of
 CC anaemias) and/or immune responses (e.g. immune response to cancer,
 CC infections or to a transplanted organ) and in identifying other members
 CC of the haematopoietin superfamily, including cytokines and receptors. The
 CC polynucleotide may be used to express recombinant protein for analysis,
 CC characterisation or therapeutic use; and as markers for tissues or
 CC chromosomes. The polypeptide and polynucleotide may also be used as
 CC nutritional sources or supplements. This is the amino acid sequence of
 CC human interleukin 21 (IL21), a cytokine receptor that can be used to
 CC characterise the novel haematopoietin receptor of the invention
 XX
 XX Sequence 162 AA;

Query Match 100.0%; Score 850; DB 7; Length 162;
 Best Local Similarity 100.0%; Pred. No. 1.3e-86;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRSSPGNMRIVICLMVIFGLTVHKSSQGGDRHMRQLIDVDQLKNYVNDLVPEF 60
 DB 1 MRSSPGNMRIVICLMVIFGLTVHKSSQGGDRHMRQLIDVDQLKNYVNDLVPEF 60
 QY 61 LPAPEDVETNCEWSAFSCFQKALKSANTGNNGRIINVSIIKKLKKPPSTNAGRQKHL 120
 DB 61 LPAPEDVETNCEWSAFSCFQKALKSANTGNNGRIINVSIIKKLKKPPSTNAGRQKHL 120
 QY 121 TCPSCDSYEKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
 DB 121 TCPSCDSYEKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162

RESULT 7
 ADE85808
 ID ADE85808 standard; protein; 162 AA.
 XX
 AC ADE85808;
 XX
 XX 29-JAN-2004 (first entry)
 XX
 DE Human interleukin-21.

XX Human; interleukin-21; immunosuppressive; antirheumatic; antiarthritic;
 KW antinflammatory; dermatological; ophthalmological; uropathic;
 KW muscular-gen.; vasotropic; antidiabetic; antithyroid; thyromimetic;
 KW neuroprotective; gastrointestinal-gen.; antipsoriatic; gene therapy.

OS Homo sapiens.
 XX WO2003087320-A2.
 XX
 XX 23-OCT-2003.
 XX
 XX 08-APR-2003; 2003WO-US010736.
 XX
 XX 09-APR-2002; 2002US-0371038P.
 XX
 XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
 XX
 XX Moll T, Strom TB, Zheng XX;
 XX WPI; 2003-845317/78.

XX New substantially pure interleukin-21 polypeptide, useful for diagnosing,
 PT treating and prognosticating autoimmune disorders, e.g. rheumatic
 PT disease, type I diabetes, Graves disease, multiple sclerosis, psoriasis
 PT and myasthenia gravis.

XX Disclosure; SEQ ID NO 1; 65pp; English.
 XX
 XX The present sequence is the protein sequence of human interleukin-21 (IL-
 CC 21). The invention provides antagonists of the IL-21 receptor. These
 CC include mutants of murine IL-21 in which the Gln residue at position 119

CC of the mature polypeptide is substituted by Asp or in which the Gln
 CC residues at positions 114 and 119 of the mature polypeptide are both
 CC replaced by Asp. The mutant IL-21 polypeptides inhibit or suppress T-cell
 CC activation. They preferably comprise a sequence that increases
 CC circulating half-life, such as the Fc region of an IgG molecule and may
 CC further comprise an antigenic tag. Such antagonists inhibit cellular
 CC proliferation in response to either anti-CD3 monoclonal antibodies or
 CC anti-CD3 antibodies applied together with IL-2 and/or IL-15 together with
 CC IL-21. A claimed method of suppressing the immune response in a patient
 CC comprises administering the IL-21 antagonist or a nucleic acid encoding
 CC it. The method is used to treat an autoimmune disease such as rheumatic
 CC disease, including systemic lupus erythematosus, Sjogren's syndrome,
 CC scleroderma, mixed connective tissue disease, dermatomyositis,
 CC polymyositis, Reiter's syndrome, or Behcet's disease, or rheumatoid
 CC arthritis, type I diabetes, autoimmune disease of the thyroid such as
 CC Hashimoto's thyroiditis or Graves' disease, an autoimmune disease of the
 CC central nervous system such as multiple sclerosis, myasthenia gravis, or
 CC encephalomyelitis, or an autoimmune disease selected from pemphigus
 CC vulgaris, pemphigus vegetans, pemphigus foliaceus, Seneear-Usher syndrome,
 CC Brazilian pemphigus, psoriasis or inflammatory bowel disease (all
 CC claimed).

XX
 XX Sequence 162 AA;
 S0
 Query Match 100.0%; Score 850; DB 7; Length 162;
 Best Local Similarity 100.0%; Pred. No. 1.3e-86;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRSSPGNMRIVICLMVIFGLTVHKSSQGGDRHMRQLIDVDQLKNYVNDLVPEF 60
 DB 1 MRSSPGNMRIVICLMVIFGLTVHKSSQGGDRHMRQLIDVDQLKNYVNDLVPEF 60
 QY 61 LPAPEDVETNCEWSAFSCFQKALKSANTGNNGRIINVSIIKKLKKPPSTNAGRQKHL 120
 DB 61 LPAPEDVETNCEWSAFSCFQKALKSANTGNNGRIINVSIIKKLKKPPSTNAGRQKHL 120
 QY 121 TCPSCDSYEKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
 DB 121 TCPSCDSYEKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162

RESULT 8
 AAE14934
 ID AAE14934 standard; protein; 162 AA.
 XX
 AC AAE14934;
 XX
 XX 27-AUG-2003 (first entry)
 XX
 DE Human interleukin-21 (IL-21) antagonist #2.
 XX
 XX Interleukin-21; IL-21; antagonist; cancer; inflammatory;
 KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
 KW systemic lupus erythematosus; myasthenia gravis; diabetes; human;
 KW zalphall ligand; mutant; mutein.

OS Homo sapiens.
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 XX Misc-difference 145 /note= "Wild-type Gln substituted with Asp"
 XX
 XX Misc-difference 148 /note= "Wild-type Ile substituted with Asp"
 XX
 XX WO2003040313-A2.
 XX
 XX 15-MAY-2003.
 XX
 XX 28-OCT-2002; 2002WO-US034502.
 XX
 XX 05-NOV-2001; 2001US-0337586P.

XX
 XX

(ZYMO) ZYMOGENETICS INC.

Presnell SR, West JW, Novak JE;

WPI; 2003-441547/41.

N-PSDB; AAD47854.

New IL-21 polypeptide and encoding polynucleotide, useful for diagnosing PT and treating disorders with aberrant expression or activity of the IL-21 PT polypeptide, such as cancer, rheumatoid arthritis, multiple sclerosis and PT diabetes.

Claim 3; Page 58; 71pp; English.

The invention relates to polynucleotides and polypeptides of interleukin-21 (IL-21) antagonists, that bind with specificity and exhibit an EC50 that is not detectable in receptor binding studies. The antagonists of the invention have mutations in the D helix of the IL-21 molecule, and can be used to inhibit the activity of IL-21 with its cognate receptor. The IL-21 antagonists are useful for diagnosing and treating disorders involving the aberrant expression or activity of the IL-21 polypeptide, such as cancer, inflammatory and autoimmune disorders, including rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus, myasthenia gravis and diabetes. The polypeptides can also be used to prepare antibodies that bind IL-21 epitopes, peptides or polypeptides, and for enhancing in vivo killing of target tissues. The present sequence is human IL-21 antagonist. The antagonist molecule is a mutant of IL-21 polypeptide, with Gln145Asp and Ile148Asp substitutions. The resulting mutant was designated zalphall ligand Q153D/1156D

Sequence 162 AA;

Query Match 97.8%; Score 831; DB 7; Length 162;

Best Local Similarity 98.1%; Pred. No. 1.7e-84;
Matches 159; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MRSPGNNRIVICLMVIFLGLTVHKSSSQQRHMRMQQLDIVDQLKNYVNDLVPEF 60
DB 1 MDSSPGNNRIVICLMVIFLGLTVHKSSSQQRHMRMQQLDIVDQLKNYVNDLVPEF 60
QY 61 LPAPEDVETNCWSAFSCFQKAQLKSANTGNRRIINVSIKLKRKPPSTNAGRQKHRL 120
DB 61 LPAPEDVETNCWSAFSCFQKAQLKSANTGNRRIINVSIKLKRKPPSTNAGRQKHRL 120
QY 121 TCPSCDSYEKKPKPEFLERFKSLLOKMHLSRTHGSEDS 162
DB 121 TCPSCDSYEKKPKPEFLERFKSLLDKMDHQLSRTHGSEDS 162

RESULT 9

AAE14933

ID AAE14933 standard; protein; 147 AA.

AC AAE14933;

XX 27-AUG-2003 (first entry)

DE Human interleukin-21 (IL-21) antagonist #1.

XX Interleukin-21; IL-21; antagonist; cancer; inflammatory;
KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
KW systemic lupus erythematosus; myasthenia gravis; diabetes; human;
KW zalphall ligand; mutant; mutein.

OS Homo sapiens.

OS Synthetic.

FH Key Location/Qualifiers

FT Misc-difference 145

/note= "Wild-type Gln substituted with Asp"

XX WO2003040313-A2.

15-MAY-2003.

28-OCT-2002; 2002WO-US034502.

05-NOV-2001; 2001US-0337586P.

(ZYMO) ZYMOGENETICS INC.

Presnell SR, West JW, Novak JE;

WPI; 2003-441547/41.

N-PSDB; AAD47853.

New IL-21 polypeptide and encoding polynucleotide, useful for diagnosing PT and treating disorders with aberrant expression or activity of the IL-21 PT polypeptide, such as cancer, rheumatoid arthritis, multiple sclerosis and PT diabetes.

Claim 3; Page 55-56; 71pp; English.

The invention relates to polynucleotides and polypeptides of interleukin-21 (IL-21) antagonists, that bind with specificity and exhibit an EC50 that is not detectable in receptor binding studies. The antagonists of the invention have mutations in the D helix of the IL-21 molecule, and can be used to inhibit the activity of IL-21 with its cognate receptor. The IL-21 antagonists are useful for diagnosing and treating disorders involving the aberrant expression or activity of the IL-21 polypeptide, such as cancer, inflammatory and autoimmune disorders, including rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus, myasthenia gravis and diabetes. The polypeptides can also be used to prepare antibodies that bind IL-21 epitopes, peptides or polypeptides, and for enhancing in vivo killing of target tissues. The present sequence is human IL-21 antagonist. The antagonist molecule is a mutant of IL-21 polypeptide, with truncation after residue 147 (Met) and Gln145Asp substitution. The resulting mutant was designated zalphall ligand I156ST/Q153D

Sequence 147 AA;

Query Match 89.2%; Score 758; DB 7; Length 147;

Best Local Similarity 98.6%; Pred. No. 2.2e-76;
Matches 145; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRSPGNNRIVICLMVIFLGLTVHKSSSQQRHMRMQQLDIVDQLKNYVNDLVPEF 60
DB 1 MDSSPGNNRIVICLMVIFLGLTVHKSSSQQRHMRMQQLDIVDQLKNYVNDLVPEF 60
QY 61 LPAPEDVETNCWSAFSCFQKAQLKSANTGNRRIINVSIKLKRKPPSTNAGRQKHRL 120
DB 61 LPAPEDVETNCWSAFSCFQKAQLKSANTGNRRIINVSIKLKRKPPSTNAGRQKHRL 120
QY 121 TCPSCDSYEKKPKPEFLERFKSLLOKM 147
DB 121 TCPSCDSYEKKPKPEFLERFKSLLDKM 147

RESULT 10

AAB18627

ID AAB18627 standard; protein; 519 AA.

XX AAB18627;

XX 22-JAN-2001 (first entry)

DE Amino acid sequence of MBP-human zalphall ligand fusion in pTAP126.

KW zalphall ligand; cytokine; haematopoietic cell proliferation; lymphoma;
KW tumorigenesis; leukaemia; hematopoiesis; B cell tumour.

OS Synthetic.

OS Homo sapiens.

XX WO200053761-A2.

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XX 14-SEP-2000.
XX
XX
XX PF 09-MAR-2000; 2000WC-US006067.
XX
XX
XX PR 09-MAR-1999; 99US-00264908.
XX
XX PR 11-MAR-1999; 99US-00265992.
XX
XX PR 01-JUL-1999; 99US-0142013P.
XX
XX
XX PA (ZYMO ) ZYMOGENETICS INC.
XX
XX
XX PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
XX PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX
XX DR WPI: 2000-565600/52.
XX DR N-PSDB; AAA75599.
XX
XX
XX PT New human cytokine, designated zalphall ligand, useful for stimulating
XX PT the proliferation and/or development of hematopoietic cells in vitro and
XX PT in vivo, and for treating tumorigenesis.
XX
XX PS Example 31; Page 233-235; 256pp; English.
XX
XX CC The present sequence represents a MBP-human zalphall ligand fusion in the
XX CC plasmid pTAP126. Zalphall ligand is a cytokine. The zalphall ligand is
XX CC useful for stimulating the proliferation and development of
XX CC haematopoietic cells in vitro and in vivo. Zalphall ligand
XX CC polynucleotides can be used as primers or probes for cloning the zalphall
XX CC gene. The zalphall ligand is useful for treating tumorigenesis. A
XX CC zalphall ligand-saporin fusion toxin may be used for treating leukaemias
XX CC and lymphomas. Antagonists against zalphall ligand are useful as research
XX CC reagents for characterizing ligand-receptor interaction. Antagonists are
XX CC also useful for inhibiting expansion, proliferation, activation and
XX CC differentiation of cells involved in regulating hematopoiesis. The
XX CC zalphall ligand may also be used to stimulate an immune response against
XX CC B cell tumour, a virus, a parasite or a bacterium. The zalphall
XX CC polypeptides, polynucleotides, antagonists, agonists and antibodies are
XX CC also useful for the detection, diagnosis, prevention, and treatment of
XX CC diseases associated with a zalphall ligand genetic defect
XX
XX SQ Sequence 519 AA;
XX
XX Query Match 81.8%; Score 695.5; DB 3; Length 519;
XX Best Local Similarity 95.7%; Pred. No. 1.1e-68;
XX Matches 134; Conservative 1; Mismatches 2; Indels 3; Gaps 1;
XX
XX QY 23 LVHKSSSQGDHMTMRQLDIVDQKNVNDLVPEFLPAPEDVETNCWSAFSCFQKA 82
XX Db 383 LVPRGS---QDRHMTRQLDIVDQKNVNDLVPEFLPAPEDVETNCWSAFSCFQKA 439
XX
XX QY 83 QLKSGANTGNRRRIINVSIKLKKRPPSTNAGRQKRLTGPCSDSYEKPKPKFLEFRPKS 142
XX Db 440 QLKSGANTGNRRRIINVSIKLKKRPPSTNAGRQKRLTGPCSDSYEKPKPKFLEFRPKS 499
XX
XX QY 143 LQKMIHQHLSRTHGSEDS 162
XX Db 500 LQKMIHQHLSRTHGSEDS 519
XX
XX RESULT 11
XX AAU11971
XX ID AAU11971 standard; protein; 519 AA.
XX
XX AC AAU11971;
XX
XX DT 09-APR-2002 (first entry)
XX
XX DE MBP-human zalphall Ligand fusion protein.
XX
XX KW Cytokine; zalphall Ligand; zalphall receptor; NK cell progenitor;
XX KW natural killer cell proliferation; T-cell proliferation; mutant;
XX KW B-cell proliferation; anti-tumour response; immune system; MBP;
XX KW immunostimulant; cytostatic; human; maltose binding protein; mutin.

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XX OS Homo sapiens.
XX OS Synthetic.
XX
XX PN US6307024-B1.
XX
XX PD 23-OCT-2001.
XX
XX PF 09-MAR-2000; 2000US-00522217.
XX
XX PR 09-MAR-1999; 99US-0123547P.
XX PR 11-MAR-1999; 99US-0123904P.
XX PR 01-JUL-1999; 99US-0142013P.
XX
XX PA (ZYMO ) ZYMOGENETICS INC.
XX
XX PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
XX PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX
XX DR WPI: 2002-040208/05.
XX DR N-PSDB; AAS20714.
XX
XX PT New zalphall ligand polypeptides and polynucleotides, useful for
XX PT stimulating proliferation, activation, differentiation and/or induction
XX PT of inhibition of specialized cell function, or for stimulating an
XX PT antigenic response.
XX
XX PS Example 31; Col 161-166; 105pp; English.
XX
XX CC The present invention relates to the isolation of a novel cytokine,
XX CC zalphall ligand and the polynucleotide encoding it. The invention also
XX CC gives the sequence for the zalphall receptor and the polynucleotide
XX CC encoding it. The zalphall ligand polypeptide stimulates proliferation of
XX CC natural killer (NK) cells or NK cell progenitors, the activation of NK
XX CC cells, proliferation of T-cells, proliferation of B-cells stimulated with
XX CC anti-CD40 antibodies, stimulates an antigenic response in a mammal, and
XX CC reduces proliferation of B-cells stimulated with anti-IGM antibodies. The
XX CC zalphall ligand polypeptide is also useful in preparing antibodies that
XX CC bind to zalphall ligand epitopes. The zalphall ligand polynucleotides can
XX CC be used as probes or primers to clone regions of a zalphall ligand gene,
XX CC and in gene therapy. Zalphall ligand may also be used to identify
XX CC inhibitors of its activity, to enhance the generation of anti-tumour
XX CC responses with or without the infusion of donor lymphocytes, and to
XX CC activate or stimulate the immune system. The present sequence
XX CC representing MBP-human zalphall Ligand fusion protein is used in the
XX CC methods of the present invention
XX
XX SQ Sequence 519 AA;
XX
XX Query Match 81.8%; Score 695.5; DB 5; Length 519;
XX Best Local Similarity 95.7%; Pred. No. 1.1e-68;
XX Matches 134; Conservative 1; Mismatches 2; Indels 3; Gaps 1;
XX
XX QY 23 LVHKSSSQGDHMTMRQLDIVDQKNVNDLVPEFLPAPEDVETNCWSAFSCFQKA 82
XX Db 383 LVPRGS---QDRHMTRQLDIVDQKNVNDLVPEFLPAPEDVETNCWSAFSCFQKA 439
XX
XX QY 83 QLKSGANTGNRRRIINVSIKLKKRPPSTNAGRQKRLTGPCSDSYEKPKPKFLEFRPKS 142
XX Db 440 QLKSGANTGNRRRIINVSIKLKKRPPSTNAGRQKRLTGPCSDSYEKPKPKFLEFRPKS 499
XX
XX QY 143 LQKMIHQHLSRTHGSEDS 162
XX Db 500 LQKMIHQHLSRTHGSEDS 519
XX
XX RESULT 12
XX AAB18624
XX ID AAB18624 standard; protein; 146 AA.
XX
XX AC AAB18624;
XX
XX DT 22-JAN-2001 (first entry)

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XX DE A mouse zalphall ligand polypeptide.
 XX DE zalphall ligand, cytokine, haematopoietic cell proliferation; lymphoma;
 KW tumorigenesis; leukaemia; hematopoiesis; B cell tumour.
 OS Mus musculus.
 PN WO200053761-A2.
 XX 14-SEP-2000.
 XX 09-MAR-2000; 2000WO-US006067.
 XX 09-MAR-1999; 99US-00264908.
 PR 11-MAR-1999; 99US-00265992.
 PR 01-JUL-1999; 99US-0142013P.
 XX (Zymo) ZYMOGENETICS INC.
 PA Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
 XX Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
 PI WPI: 2000-565600/52.
 DR N-PSDB; AAA75580.
 XX New human cytokine, designated zalphall ligand, useful for stimulating
 PT the proliferation and/or development of hematopoietic cells in vitro and
 PT in vivo, and for treating tumorigenesis.
 XX Disclosure; Page 222-223; 256pp; English.
 XX The present sequence represents a mouse zalphall ligand polypeptide,
 CC which is a cytokine. The zalphall ligand is useful for stimulating the
 CC proliferation and development of haematopoietic cells in vitro and in
 CC vivo. Zalphall ligand polynucleotides can be used as primers or probes
 CC for cloning the zalphall gene. The zalphall ligand is useful for treating
 CC tumorigenesis. A zalphall ligand-epoxin fusion toxin may be used for
 CC treating leukaemias and lymphomas. Antagonists against zalphall ligand
 CC are useful as research reagents for characterizing ligand-receptor
 CC interaction. Antagonists are also useful for inhibiting expansion,
 CC proliferation, activation and differentiation of cells involved in
 CC regulating hematopoiesis. The zalphall ligand may also be used to
 CC stimulate an immune response against B cell tumour, a virus, a parasite
 CC or a bacterium. The zalphall polypeptides, polynucleotides, antagonists,
 CC agonists and antibodies are also useful for the detection, diagnosis,
 CC prevention, and treatment of diseases associated with a zalphall ligand
 CC genetic defect
 XX Sequence 146 AA;
 SQ Query Match 57.2%; Score 486; DB 3; Length 146;
 Best Local Similarity 63.0%; Pred. No. 5.6e-46;
 Matches 92; Conservative 23; Mismatches 31; Indels 0; Gaps 0;
 QY 8 MERIVICLVIFLGTVAHSSQGDHIRMRLIDIVDQKKNYNDLVPEFLPAPEDV 67
 DB 1 MERIVICLVIFLGTVAHSSQGDHIRMRLIDIVDQKKNYNDLVPEFLPAPEDV 60
 QY 68 ETNCEWAFSCFQAKLKSANTGNRIINYSIKLKRKPPSTNAGRQKHRLTCSDCS 127
 DB 61 KGHCEHAAPACFQAKLKPSNPGNKTFTIDLVAQLRRRLPARRGGKKQKHIAKCPSCDS 120
 QY 128 YEKPPKPEFLERFKSLQKMIHQHLS 153
 DB 121 YEKPTPEFLERLKLWLLQKMIHQHLS 146
 RESULT 13
 AA013737
 ID AA013737 standard; protein, 146 AA.
 XX AA013737
 AC AA013737

XX DT 26-FEB-2002 (first entry)
 XX DE Murine soluble Zalphall cytokine receptor ligand.
 XX DE Murine, Zalphall, cytokine receptor; immunosuppressive; cytostatic;
 KW inflammatory disorder; haemostatic; cell proliferation; immune disorder;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
 KW myasthenia gravis; systemic lupus erythematosus; SLE; diabetes; asthma;
 KW ulcerative colitis; inflammatory bowel disease; Crohn's disease; sepsis;
 KW viral infection.
 XX OS Mus musculus.
 XX WO200177171-A2.
 XX 18-OCT-2001.
 XX 03-APR-2001; 2001WO-US010872.
 XX 05-APR-2000; 2000US-0194731P.
 PR 28-JUL-2000; 2000US-0222121P.
 XX (Zymo) ZYMOGENETICS INC.
 PA Sprecher CA, Novak JE, West JW, Presnell SR, Holly RD, Nelson AJ;
 XX WPI: 2002-025898/03.
 DR N-PSDB; AAD22952.
 XX Novel soluble receptor polypeptides and polynucleotides used as cytokine
 PT antagonist for stimulating ligand activity-induced proliferation of
 PT hematopoietic cells and for suppressing immune response in a mammal.
 XX Claim 1; Page 212; 243pp; English.
 XX The invention relates to an isolated soluble zalphall cytokine receptor
 CC polypeptide and their cDNA molecules. Zalphall proteins are useful for
 CC inhibiting or antagonising the ligand activity-induced proliferation of
 CC haematopoietic cells and haematopoietic cell progenitors preferably
 CC lymphoid cells which are natural killer cells or cytotoxic T cells.
 CC Zalphall is useful for treating immune and inflammatory disorders, for
 CC reducing proliferation of neoplastic B or T cells, for suppressing an
 CC immune response in a mammal exposed to an antigen or pathogen. Zalphall is
 CC useful for treating diseases that require immune regulation including
 CC autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,
 CC myasthenia gravis, systemic lupus erythematosus (SLE) and diabetes;
 CC asthma, ulcerative colitis, inflammatory bowel disease, Crohn's disease,
 CC sepsis, viral infection (dengue virus infection) and cancer. The present
 CC sequence is murine soluble Zalphall cytokine receptor ligand
 XX Sequence 146 AA;
 SQ Query Match 57.2%; Score 486; DB 5; Length 146;
 Best Local Similarity 63.0%; Pred. No. 5.6e-46;
 Matches 92; Conservative 23; Mismatches 31; Indels 0; Gaps 0;
 QY 8 MERIVICLVIFLGTVAHSSQGDHIRMRLIDIVDQKKNYNDLVPEFLPAPEDV 67
 DB 1 MERIVICLVIFLGTVAHSSQGDHIRMRLIDIVDQKKNYNDLVPEFLPAPEDV 60
 QY 68 ETNCEWAFSCFQAKLKSANTGNRIINYSIKLKRKPPSTNAGRQKHRLTCSDCS 127
 DB 61 KGHCEHAAPACFQAKLKPSNPGNKTFTIDLVAQLRRRLPARRGGKKQKHIAKCPSCDS 120
 QY 128 YEKPPKPEFLERFKSLQKMIHQHLS 153
 DB 121 YEKPTPEFLERLKLWLLQKMIHQHLS 146
 RESULT 14
 AA011968
 ID AA011968 standard; protein, 146 AA.

XX AAU11968;
 XX AC
 XX DT
 XX DE
 XX DE Mouse zalphall Ligand polypeptide.
 XX KW Cytokine; zalphall Ligand; zalphall receptor; NK cell progenitor;
 XX KW natural killer cell proliferation; T-cell proliferation;
 XX KW B-cell proliferation; anti-tumour response; immune system;
 XX KW immunostimulant; cytostatic; mouse.
 XX OS Mus musculus.
 XX PN US6307024-B1.
 XX PD 23-OCT-2001.
 XX PF 09-MAR-2000; 2000US-00522217.
 XX PR 09-MAR-1999; 99US-0123547P.
 XX PR 11-MAR-1999; 99US-0123904P.
 XX PR 01-JUL-1999; 99US-0142013P.
 XX PA (ZYMO) ZYMOGENETICS INC.
 XX PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
 XX PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
 XX DR WPI: 2002-040208/05.
 XX DR N-PSDB; AAS20688.
 XX PT New zalphall ligand polypeptides and polynucleotides, useful for
 XX PT stimulating proliferation, activation, differentiation and/or induction
 XX PT of inhibition of specialized cell function, or for stimulating an
 XX PT antigenic response.
 XX PS Example 16; Col 147-150; 105pp; English.
 XX CC The present invention relates to the isolation of a novel cytokine,
 XX CC zalphall Ligand and the polynucleotide encoding it. The invention also
 XX CC gives the sequence for the zalphall receptor and the polynucleotide
 XX CC encoding it. The zalphall ligand polypeptide stimulates proliferation of
 XX CC natural killer (NK) cells or NK cell progenitors, the activation of NK
 XX CC cells, proliferation of T-cells, proliferation of B-cells stimulated with
 XX CC anti-CD40 antibodies, stimulates an antigenic response in a mammal, and
 XX CC reduces proliferation of B-cells stimulated with anti-IgM antibodies. The
 XX CC zalphall Ligand polypeptide is also useful in preparing antibodies that
 XX CC bind to zalphall Ligand epitopes. The zalphall Ligand polynucleotides can
 XX CC be used as probes or primers to clone regions of a zalphall Ligand gene,
 XX CC and in gene therapy. Zalphall Ligand may also be used to identify
 XX CC inhibitors of its activity, to enhance the generation of anti-tumour
 XX CC responses with or without the infusion of donor lymphocytes, and to
 XX CC activate or stimulate the immune system. The present sequence represents
 XX CC mouse zalphall Ligand polypeptide
 XX CC
 XX CC Sequence 146 AA;
 XX CC
 XX CC Query Match 57.2%; Score 486; DB 5; Length 146;
 XX CC Best Local Similarity 63.0%; Pred No. 5.6e-46;
 XX CC Matches 92; Conservative 23; Mismatches 31; Indels 0; Gaps 0;
 Y 8 MERIVCLMVFILGTLVHKSSQGGDRMIRMRQLIDVQLKYNVNDLPFLPAPDV 67
 b 1 MERTLLVVFILGTVLHKSSQGGDRLLIRLRLHLDIVELQKTYENDLPFLSAPQDV 60
 Y 68 ETNCEWSAFSCFQKALQSANTGNNEIRINVISIKLKKPPSTNAGROKHLTCCSCDS 127
 b 61 KGECEHARACFKKALKPSFNENKNTLIDVQLRLRLPARGGKKQKHIAKPCSDS 120
 Y 128 YKKPPEFLERFKSLLOKQIHQLS 153
 b 121 YKRTPEFLERLKLWLLQKQIHQLS 146

RESULT 15

AD85809
 ID AD85809 standard; protein; 146 AA.

XX AC AD85809;

XX DT 29-JAN-2004 (first entry)

XX DE Murine interleukin-21.

XX KW Mouse; interleukin-21; immunosuppressive; antirheumatic; antiarthritic;
 XX KW antinflammatory; dermatological; ophtalmological; uropathic;
 XX KW muscular-gen.; vasotropic; antidiabetic; antithyroid; thyromimetic;
 XX KW neuroprotective; gastrointestinal-gen.; antipsoriatic; gene therapy.

XX OS Mus sp.

XX PN WO2003087320-A2.

XX PD 23-OCT-2003.

XX PF 08-APR-2003; 2003WO-US010736.

XX PR 09-APR-2002; 2002US-0371038P.

XX PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

XX PI Moll T, Strom TB, Zheng XX;

XX WPI: 2003-845317/78.

XX New substantially pure interleukin-21 polypeptide, useful for diagnosing,
 XX PT treating and prognosticating autoimmune disorders, e.g. rheumatic
 XX PT disease, type I diabetes, Graves disease, multiple sclerosis, psoriasis
 XX PT and myasthenia gravis.

XX PS Claim 1; SEQ ID NO 2; 65pp; English.

XX The present sequence is the protein sequence of murine interleukin-21 (IL
 XX -21). The invention provides antagonists of the IL-21 receptor. These
 XX include mutants of murine IL-21 in which the Gln residue at position 119
 XX of the mature polypeptide is substituted by Asp AD85806 or in which the
 XX Gln residues at positions 114 and 119 of the mature polypeptide are both
 XX replaced by Asp AD85807. The mutant IL-21 polypeptides inhibit or
 XX suppress T-cell activation. They preferably comprise a sequence that
 XX increases circulating half-life, such as the FC region of an IgG molecule
 XX and may further comprise an antigenic tag. Such antagonists inhibit
 XX cellular proliferation in response to either anti-CD3 monoclonal
 XX antibodies or anti-CD3 antibodies applied together with IL-2 and/or IL-15
 XX together with IL-21. A claimed method of suppressing the immune response
 XX in a patient comprises administering the IL-21 antagonist or a nucleic
 XX acid encoding it. The method is used to treat an autoimmune disease such
 XX as rheumatic disease, including systemic lupus erythematosus, Sjogren's
 XX syndrome, scleroderma, mixed connective tissue disease, dermatomyositis,
 XX polymyositis, Reiter's syndrome, or Behcet's disease, or rheumatoid
 XX arthritis, type I diabetes, autoimmune disease of the thyroid such as
 XX Hashimoto's thyroiditis or Graves' disease, an autoimmune disease of the
 XX central nervous system such as multiple sclerosis, myasthenia gravis, or
 XX encephalomyelitis, or an autoimmune disease selected from pemphigus
 XX vulgaris, pemphigus vegetans, pemphigus foliaceus, Senechal-Usher syndrome,
 XX Brazilian pemphigus, psoriasis or inflammatory bowel disease (all
 XX claimed).

XX Sequence 146 AA;

XX Query Match 57.2%; Score 486; DB 7; Length 146;

XX Best Local Similarity 63.0%; Pred. No. 5.6e-46;

XX Matches 92; Conservative 23; Mismatches 31; Indels 0; Gaps 0;

XX QY 8 MERIVCLMVFILGTLVHKSSQGGDRMIRMRQLIDVQLKYNVNDLPFLPAPDV 67

